

LEONARDO PAES DA SILVA

SULFONAMIDES DERIVED FROM ANACARDIC ACID AS POTENTIAL ANTICHAGASIC: A THEORETICAL APPROACH BASED ON MOLECULAR DOCKING, MOLECULAR DYNAMICS, AND DENSITY FUNCTIONAL THEORY CALCULATIONS

FORTALEZA

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Dissertação apresentada ao Programa de Pós-Graduação em Química da Universidade Federal do Ceará como requisito parcial à obtenção do título de mestre em Química. Área de concentração: Físico-Química.

Orientador: Prof. Dr. Pedro de Lima Neto. Coorientador: Prof. Dr. Emmanuel Silva Marinho.

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To God, my parents, and friends.

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I recognize my insignificance, and in front of the LORD, I owe gratitude for my life and for giving me the opportunity to fulfill my mission each day.

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"Coragem fez de mim, um grande lutador Mesmo sendo sofredor acredito no amor Amor de um homem que andou pegando a paz Jejuou no deserto, falou não pro Satanás Aquele ali sim, teve determinação Não fraquejou com os irmãos Você sabe, tem vários por aí que são covarde Usa da maldade, falta com verdade Final dos tempos está se aproximando Falta fé, cresce o ódio, assim vive o ser humano" (Sabotage)

ABSTRACT

Chagas disease (CD) is a tropical disease caused by the parasite Trypanosoma cruzi, transmitted by the barber insect. Currently, there are approximately 7 million infected people in the world, and it is estimated that 70 million people could contract this disease. The anacardic acid (AA) showed effectiveness in silico and in vivo tests. The antichagasic potential of five sulfonamide molecules, derived from anacardic acid, was evaluated from a molecular approach based on Density Functional Theory (DFT), Molecular Dynamics (MD), and Molecular Docking calculations. Methyl 2-methoxy-6- (8- (methylsulfonamide) octyl) benzoate (SA1); 2-methoxy-6- (8- (phenylsulfonamide) octyl) benzoate (SA2); methyl 2-methoxy-6- (8- (2methylphenyl sulfonamide) octyl) benzoate (SA3); methyl 2-methoxy-6-(8-(methylphenylsulfonamide)octyl)benzoate (SA4); methyl2-(8-(2,5-

dimethylphenylsulfonamide)octyl)-6-methoxybenzoate (SA5) were the investigated molecules. The DFT calculations were performed using the B3LYP/6-311+G (d, p) level of theory. The global and local reactivity data showed that SA1 shows the highest molecular reactivity, while SA2 is the most stable derivative. In addition, the structures of investigated molecules were confirmed by the linear correlations higher than 0.98 displayed between the experimental and calculated spectroscopic data (IR and NMR). Molecular docking of the molecules showed a greater prominence for the SA1, SA2, and SA4 molecules in the results of distances of ligand/cruzain. In molecular dynamics, SA4 obtained better stability due to greater interactions with important aminoacids of cruzain.

Keywords: sulfonamide; density functional theory; molecular docking; molecular dynamics.

RESUMO

A doença de Chagas é uma doença tropical causada pelo parasito Trypanosoma cruzi, transmitida pelo inseto barbeiro. Atualmente, há aproximadamente cerca 7 milhões de pessoas infectadas no mundo, além disso, calcula-se que 70 milhões de pessoas poderão contrair essa doença. O ácido anacárdico (AA) mostrou efetividade em teste em teste in sílico e in vivo. O potencial antichagásico de cinco moléculas sulfonamidas, derivadas do ácido anacárdico, foi avaliado o potencial reativo dos derivados moléculas em uma abordagem molecular baseada na Teoria Funcional da Densidade (DFT). Na Dinâmica molecular (MD) e nos cálculos de Docking molecular foi verificado a interação desses derivados, com a enzima alvo (cruzaína). Metil 2-metoxi-6- (8-(metilsulfonamida) octil) benzoato (SA1); Metil 2-metoxi-6-(8-(fenilsulfonamida) octil) benzoato (SA2); Metil 2-metoxi-6- (8- (2-metilfenil sufonamida) octil) benzoato (SA3); metil 2-metoxi-6- (8- (metilfenilsulfonamida) octil) benzoato (SA4); metil 2- (8- (2,5- dimetilfenilsulfonamida) octil) -6-metoxibenzoato (SA5) foram as moléculas investigadas. Os cálculos do DFT foram realizados utilizando o nível teórico B3LYP/6-311+G (d, p). As estruturas das moléculas investigadas foram confirmadas pelas correlações lineares superiores a 0,98 entre os dados espectroscópicos experimentais calculados de Infravermelho (IV) e Ressonância Magnética Nuclear (RMN) do carbono. Os dados de reatividade global e local mostraram que SA1 mostra a maior reatividade molecular, enquanto SA2 é a derivada mais estável. Além disso, o Docking molecular das moléculas mostrou destaques para as moléculas SA1, SA2 e SA4 nos resultados das distâncias de interação ligante/cruzaína, e no desempenho da dinâmica molecular, SA4 obteve melhor estabilidade com o sítio, devido a uma maior quantidade de interações com importantes aminoácidos da cruzaína.

Palavras-chave: sulfonamida; teoria do funcional da densidade; docking molecular; dinâmica molecular.

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LIST OF ABBREVIATIONS AND ACRONYMS

AA	Anacardic Acid
Ala	Alanine
Asn	Asparagine
BZN	Benznidazol
Cys	Cysteine
DFT	Density Functional Theory
Gln	Glutamine
Gly	Glycine
Gromacs	Groningen Machine for Chemical Simulation
His	Histidine
Lys	Lysine
MD	Molecular Dynamics
Met	Methionine
PLIP	Protein-Ligand Interaction Profile
PDB	Protein Data Bank
RMSD	Root MeanSquare Deviation
SA1	Methyl 2- methoxy-6- (8- (methylsulfonamide) octyl) benzoate
SA2	Methyl 2-methoxy-6- (8- (phenylsulfonamide) octyl) benzoate
SA3	Methyl 2-methoxy-6- (8- (2methylphenylsulfonamide)octyl)benzoate
SA4	Methyl 2-methoxy-6-(8- (methylphenylsulfonamido)octyl) benzoate
SA5	Methyl 2-(8-(2,5- dimethylphenylsufonamido)octyl)-6-methoxybenzoate
Trp	Tryptophan
Val	Valine

VS1 Vinyl Sulfone I

SUMMARY

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1 INTRODUCTION

Neglected diseases are endemic tropical diseases that prevail under poverty conditions and help maintain inequality because they are potent obstacles to national development (POSENATO; LUÍS, *et al.*, [S.d.]). They mainly affect the poor in Africa, Asia, and Latin America. As examples of neglected diseases, we can mention dengue fever, Chagas disease, schistosomiasis, leishmaniasis, malaria, tuberculosis. According to the World Health Organization (WHO), more than 1 billion people are infected with one or more neglected diseases, representing one-one-sixth of the world's population. Together they cause 500,000 to 1 million deaths each year. Although funding has been provided for research related to neglected diseases, the knowledge generated has not been translated into advances in treatments such as new drugs, diagnostic methods, and vaccines ("Doenças negligenciadas: estratégias do Ministério da Saúde", 2010). One of the reasons for this is that the pharmaceutical industry's interest in the topic is low, the reason being that the profitability potential of the industry is low because the affected population is low-income, and most of them are in developing countries (BRITO; FALCÃO, *et al.*, 2021).

Despite the growing demand for safe and effective medicines, neglected diseases represent a low priority for the pharmaceutical industry. Low investment in research and development (R&D) results in few drugs and vaccines for neglected diseases. Moreover, many of the drugs were developed more than half a century ago and are highly toxic (KESSELHEIM, 2019).

Chagas Disease (CD) is caused by human infection with the protozoan *Trypanosoma cruzi* (*T. cruzi*). Insects called " blood-sucking insect " are the primary vectors involved in the spread of this disease. The infection mainly occurs by inoculating the bite site with protozoa present in the insect intestine. However, there are other forms of transmission. This disease can also be transmitted orally through food contaminated by parasites, mainly its feces (WHO).

CD is identified with an acute phase lasting about two months. The symptoms of this phase include fever, inflammation at the inoculation site, unilateral eyelid edema, lymphadenopathy, and hepatosplenomegaly(BRITO *et al.*, 2021). In addition, a high number of parasites circulate in the blood, but symptoms are absent or mild and nonspecific in most cases. In the chronic phase, parasites are mainly hidden in the heart and digestive muscles. As a result, as many as 30% of patients have heart disease, and up to 10% have digestive system disease (usually enlarged esophagus or colon), neurological disease, or mixed disease. In

addition, the infection can cause sudden death due to arrhythmia or progressive heart failure caused by the destruction of the myocardium and its nervous system(MARTINS-MELO *et al.*, 2014).

There are treatments available for CD. Benznidazole (BZN) and Nifurtimox are commonly recommended. In Brazil, where the infected population is equivalent to 4.6 million people with *T. cruzi* infection (MARTINS-MELO, RAMOS, *et al.*, 2014), the only available drug is BZN. This drug is almost 100% effective in curing the disease if administered soon after infection at the beginning of the acute phase, including cases of congenital transmission (WHO). However, BZN is effective in the chronic phase of the disease. In addition, the most common side effects are rash, digestive intolerance, anorexia, asthenia, headache, and sleep disturbances (FERREIRA, *et al.*, 2019). In more severe cases, skin reactions, fever, atopic dermatitis, erythematosus, light-sensitive rashes, purpura, weight loss, and gastrointestinal disturbances occur within the first weeks of treatment (CLAYTON, 2010).

More and more researches are being done into the use of natural medicines that effectively treat and cure diseases. Natural products have shown great potential as drugs (CHEUKA, MAYOKA, *et al.*, 2016). Natural drugs are being studied for the treatment of CD, and one of the examples is *Lychnophora trichocarpha*, a native plant from Brazilian savanna (Cerrado), indicating results in decreasing the amount of *T.cruzi* in the host's blood(SÜLSEN, PUENTE, *et al.*, 2016).

Alternatively, the use of cashew tree derivatives *Anacardium occidentale L* has been gaining space for potential drugs. Studies indicate good results as antidiabetic (JAISWAL, *et al.*, 2017; SU, *et al.*, 2019), antioxidant, larvicidal e antiacetylcholinesterase (OLIVEIRA, *et al.*, 2011), antimicrobial (K., H. *et al.*, 2014) e antifungal(SANTOS, *et al.*, 2011). The anacardic acid (AA) is one of the main components of the cashew nut shell liquid (CNSL) (PAULA, *et al.*, 2020), can be utilized as a sub-product of industrial residues. Furthermore, besides showing promising results as an antioxidant for biofuels (PAULA, *et al.*, 2020, RANGEL, *et al.*, 2021), the AA has also been shown to have biological activities, showing promising results in enzyme inhibition of Glyceraldehyde 3-phosphate (GAPDH) of *T. cruzi*, an enzyme essential of the glycolytic pathway of the antichagasic parasite, in tests with the evolutive forms of the parasite, in epimastigotes and trypomastigotes (ALVES, 2018).

Furthermore, computational resources significantly contribute to searching for new potential candidates to combat the disease (DE AZEVEDO JR., 2010). In the works of Marinho (MARINHO, *et al.*, 2019; MARINHO, *et al.*, 2020; MARINHO, *et al.*, 2021), they showed the pharmacological potential of AA as an antichagasic through molecular docking. The studies

showed an excellent interaction of AA with the enzyme cruzain, responsible for the proteolytic activity involved in several vital processes and are present in all stages of the evolutionary cycle of the parasite. It was also evaluated in silico the interaction of AA with the enzyme TcGAPHD. In the glycolytic pathway of the parasite, this enzyme is responsible for the conversion of glyceraldehyde-3-phosphate into 1,3-bisphosphoglycerate in the presence of nicotinamide adenine dinucleotide (NAD)+ inorganic phosphate (MARINHO; *et al.*, 2019; ZINSSER, *et al.*, 2014).

In a study by Reddy (REDDY; *et al.*, 2012), synthesis, Infrared (IR), and Nuclear Resonance Magnetic (NMR) spectroscopical identifications of C-8 sulfonamide derivatives of anacardic acid were performed. They showed their antibacterial activity on *Escherichia coli*, *Pseudomonas aeruginosa*, *Staphylococcus aureus* and *Streptococcus pyogenes bacterial strains*.

In this perspective, this work aims to investigate the antichagasic potential of anacardic acid sulfonamide derivatives, characterizing their global and local reactivity by the density functional theory method. Furthermore, to identify the possible sites of reactivity of these molecules with cruzain and investigate the stability of the interactions of SA1-SA5 molecules with cruzain sites through molecular dynamics, comparing them with the drug BZN.

Chapter 1

Sulfonamides derived from anacardic acid as potential antichagasic: a theoretical approach based on Molecular Docking, Molecular Dynamics, and Density Functional Theory calculations



Physical Chemistry Chemical Physics



Sulfonamide derived from anacardic acid as potential antisores: a theoretical approach based on Molecular Docking, Molecular Dynamics, and Density Functional Theory calculations

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RESUMO

A doença de Chagas é uma doença tropical causada pelo parasito Trypanosoma cruzi, transmitida pelo inseto barbeiro. Atualmente, há aproximadamente cerca 7 milhões de pessoas infectadas no mundo, além disso, calcula-se que 70 milhões de pessoas poderão contrair essa doenca. O ácido anacárdico (AA) mostrou efetividade em teste em teste in sílico e in vivo.O potencial antichagásico de cinco moléculas sulfonamidas, derivadas do ácido anacárdico, foi avaliado o potencial reativo dos derivados moléculas em uma abordagem molecular baseada na Teoria Funcional da Densidade (DFT). Na Dinâmica Molecular (MD) e nos cálculos de Docking molecular foi verificado a interação desses derivados, com a enzima alvo (cruzaína). Metil 2-metoxi-6- (8-(metilsulfonamida) octil) benzoato (SA1); Metil 2-metoxi-6-(8-(fenilsulfonamida) octil) benzoato (SA2); Metil 2-metoxi-6- (8- (2-metilfenil sufonamida) octil) benzoato (SA3); metil 2-metoxi-6- (8- (metilfenilsulfonamida) octil) benzoato (SA4); metil 2- (8- (2,5- dimetilfenilsufonamida) octil)-6-metoxibenzoato (SA5) foram as moléculas investigadas. Os cálculos do DFT foram realizados utilizando o nível teórico B3LYP/6-311+G (d, p). As estruturas das moléculas investigadas foram confirmadas pelas correlações lineares superiores a 0,98 entre os dados espectroscópicos experimentais calculados de Infra-Vermelho (IV) e Ressonancia Magnética Nuclear (RMN) do Carbono. Os dados de reatividade global e local mostram que SA1 mostra a maior reatividade molecular, enquanto SA2 é a derivada mais estável. Além disso, o Docking molecular das moléculas mostrou destaques para as moléculas SA1, SA2 e SA4 nos resultados das distâncias de interação ligante/cruzaína, e no desempenho da dinâmica molecular, SA4 obteve melhor estabilidade com o sítio, devido a uma maior quantidade de interações com importantes aminoácidos da cruzaína.

Palavras-chave Sulfonamida; Teoria do Funcional da Densidade; Docking Molecular; Dinâmica Molecular.

ABSTRACT

Chagas disease (CD) is a tropical disease caused by the parasite Trypanosoma cruzi, transmitted by the barber insect. Currently, there are approximately 7 million infected people in the world, and it is estimated that 70 million people could contract this disease. The anacardic acid (AA) showed effectiveness *in silico* and *in vivo* tests. The antichagasic potential of five sulfonamide molecules, derived from anacardic acid, was evaluated from a molecular approach based on Density Functional Theory (DFT), Molecular Dynamics (MD), and Molecular Docking (docking) calculations. Methyl 2-methoxy-6- (8- (methylsulfonamide) octyl) benzoate (SA1); 2-methoxy-6- (8- (phenylsulfonamide) octyl) benzoate (SA2); methyl 2-methoxy-6- (8- (methylphenyl sulfonamide) octyl) benzoate (SA3); methyl 2-methoxy-6- (8- (methylphenyl sulfonamide) octyl) benzoate (SA4); methyl2-(8-(2,5-

dimethylphenylsulfonamide)octyl)-6-methoxybenzoate (SA5) were the investigated molecules. The DFT calculations were performed using the B3LYP/6-311+G (d, p) level of theory. The structures of investigated molecules were confirmed by the linear correlations higher than 0.98 displayed between the experimental and calculated spectroscopic data (IR and NMR). The global and local reactivity data showed that SA1 shows the highest molecular reactivity, while SA2 is the most stable derivative. In addition, the molecular docking of the molecules showed a greater prominence for the SA1, SA2, and SA4 molecules in the results of distances of ligand/cruzain. In molecular dynamics, SA4 obtained better stability due to greater interactions with important amino acids of cruzain.

Keywords Sulfonamide; Density Functional; Molecular Docking; Molecular Dinamics.

1 Introduction

In 21 countries in Latin America, the World Health Organization (WHO) considers Chagas disease to be endemic, affecting Asia and Africa.(SCHMUNIS, 2007) WHO estimates that between six and seven million people are infected with the parasite called *Trypanosoma cruzi* (*T. cruzi*). The Chagas disease is one of the leading causes of heart disease in Latin America, and the bite transmits it by the blood-sucking insect known as Triatominae, or "kissing bugs." The parasite can evade the host's defense system through its antioxidant enzymes; increase in B lymphocytes, Hypergammaglobulinemia, and production of antibodies that do not help in the parasite cancellation, the existence of specific molecules in the parasite's membrane that also help in the inefficiency of the host's defense system in fighting the parasite.(CARDOSO; REIS-CUNHA; BARTHOLOMEU, 2016)

Some molecules are used to combat disease wounds. Among them, benznidazole is commonly used. Although this antichagasic drug was developed over 50 years ago, its mechanism of action is not yet fully discovered. It may work by covalent modification of macromolecules by nitroreducted intermediates or other nitroreducted interactions with parasite components. (OLIVEIRA *et al.*, 2008) However, it leads to several side effects for the user, which include skin reactions, fever, atopic dermatitis, erythematosus, light-sensitive rashes, purpura, weight loss, and gastrointestinal disorders, hypersensitivity symptoms, dermatitis with rash, generalized fever with edema, lymphadenopathy, muscle, and joint pain, bone marrow depression, thrombocytopenic purpura and agranulocytosis, the most severe manifestation, polyneuropathy, paresthesia and polyneuritis of the peripheral nerves.(COURA; DE CASTRO, 2002) For these reasons, alternative sources of antichagasic drugs are sought, which perform well, causing less risk to the patient.

According to the Food and Agriculture Organization (FAO), in the years 2016 and 2017, around 8 million tons of cashew nuts were produced worldwide, and 5.7 million hectares were used for production worldwide, (PAULA *et al.*, 2020) wherefrom cashew nuts phenolic compounds can be obtained, such as cardol, cardanol and Anarcardic Acid (AA). The AA, one of the main constituents of cashew nuts, is a potential candidate for antichagasic activity since tests with the evolutionary forms of *T. cruzi* epimastigotes and trypomastigotes of trypanocidal activity showed results in inhibition of essential enzymes in the evolutionary cycle of *T. cruzi*.(HAMAD; MUBOFU, 2015; MARINHO *et al.*, 2019; MUROI; KUBO, 1996; PEREIRA *et al.*, 2008) One of these enzymes is cruzain, primarily responsible for the proteolytic activity

involving several vital processes, such as host cell infection, replication, and metabolism during the parasite's life cycle.(MARINHO, 2020)

Besides, new easy-to-use syntheses of the Sulfonamide family (SA) were performed, where they are directly derived from (AA), in which they showed antibacterial activity (*viz. E. coli (MTCC443)*), *P. aeruginosa (MTCC424), S. aureus (MTCC96) e S. pyogenes (MTCC443)*.(REDDY *et al.*, 2012) In addition to their biological activities such as gastric protection, antitumor, antioxidant, antibiotics, antimicrobial activity, and soy lipoxygenase-1 inhibitory activity.(HAMAD; MUBOFU, 2015; KUBO et al., 1993)

Computational studies on molecules are a way of predicting an application as an antichagasic, in which through simulations, properties that corroborate its applicability can be obtained.(MARINHO *et al.*, 2019) Therefore, the study of the following molecules: methyl 2-methoxy-6- (8- (methylsulfonamide) octyl) benzoate (SA1); 2-methoxy-6- (8- (phenylsulfonamide) octyl) benzoate (SA2); methyl 2-methoxy-6- (8- (2methylphenyl sufonamide) octyl) benzoate (SA3); methyl 2-methoxy-6- (8- (methylphenylsulfonamide) octyl) benzoate (SA4); methyl2-(8-(2,5-dimethylphenylsulfonamide)octyl)-6 methoxybenzoate (SA5), checking their interactions with the enzyme cruzain , which is primarily responsible for a proteolytic activity involving several essential processes in the process of parasite internalization into mammalian cells, playing an important role.

Therefore, using the Density Functional Theory (DFT), a comparison was made about the global reactivities of each molecule (ionic potential, electro-affinity, Gap, electronegativity, global hardness, Softness, global electrophilicity). Also, the local reactivity, verified by the functions of the Electronic Fukui. In Molecular Docking and Molecular Dynamics (MD), the cruzain enzyme was used. Through MD simulations, it is possible to obtain the interaction between SA's molecules and cruzain their active site.

2 Materials

2.1 Quantum chemical calculations

To determine the optimized molecular geometry of the molecules was utilized, the microspecies majority was checked at pH 7.4 in MarvinSketch 18.30 version using a calculation plugin for achieving the lowest energy conformer.(CSIZMADIA, 2019) The Density Functional Theory (DFT) method was carried out in the Gaussian 09 program(FRISCH *et al.*,

2009) using Becke's three-parameter hybrid functional and the Lee, Yang, and Parr correlation functional (B3LYP)(BECKE, 1993) with the basis set triple zeta of Pople with polarization in the d and p atomic orbitals and a diffuse functions for the non-hydrogen atoms 6-311+G(d, p). After the geometrical optimization, the fundamental vibrational spectra were computed at the same level of theory to confirm that all the obtained molecular geometries can be used to determine the molecular properties of the compounds SA1-SA5 with the absence of negative vibrational frequencies, were theoretically assigned using the scaling factor of 0.9679 in the calculated wavenumbers, (ALMEIDA-NETO et al., 2020; ANDERSSON; UVDAL, 2005) confirming the state of minimum energy. Then, the ¹H and ¹³C NMR spectra were computed at B3LYP/6-311+G (d, p) level of theory in Chloroform an implicit solvent using the Polarizable Continuum Model with the Integral Equation Formalism (IEF-PCM)(DITCHFIELD; HEHRE; POPLE, 1971; MCWEENY, 1962; WOLINSKI; HINTON; PULAY, 1990) solvation model available in Gaussian 09. The tetramethylsilane (TMS) was used as a reference compound to compute the chemical shift for the carbon (δ_c) atoms using the following expressions: $\delta_c =$ $\sigma_{H(TMS)} - \sigma_{H(calc)}$, where the quantity σ_c are the calculated shielding constant for the carbon To understand the chemical behavior of the compounds, the energies of the Frontier Molecular Orbitals (FMO) were computed at B3LYP/6-311+G (d, p) computational performed with the dielectric constant of water, with the IEF-PCM solvation model. From this calculation, the energy value of these molecular orbitals was used to calculate the quantum reactivity descriptors(FUKUI, 1982): the HOMO-LUMO energy gap (ΔE_{gap} , equation 1); By Koopamns' theorem, (KOOPMANS, 1934) the ionization potential (I, equation 2) and the electron affinity (A, equation 3); From the work of Chermette; Iczkowski and Margrave, (CHERMETTE, 1999; ICZKOWSKI; MARGRAVE, 1961) the electronegativity (χ , equation 4); In Pearson's work, the global hardness (η , equation 5), and the global softness (S, equation 6) that was proposed by Yang and Parr; (YANG; PARR, 1985) The global electrophilicity index (ω , equation 7) introduced by Parr and Szentpály(PARR; SZENTPÁLY; LIU, 1999) and the global nucleophilicity index (ε , equation 8) proposed in the work of Chattaraj.(PARR; CHATTARAJ, 1991)

$$\Delta E_{GAP} = E_{LUMO} - E_{HOMO}$$
(1)

$$I = -E_{HOMO}$$
(2)

$$A = -E_{LUMO}$$
(3)

г

$$\chi = \frac{I+A}{2} \tag{4}$$

$$\eta = \frac{I - A}{2} \tag{5}$$

$$\sigma = \frac{1}{\eta}$$
(6)
$$\omega = \frac{\chi^2}{2\eta}$$
(7)
$$\varepsilon = \frac{1}{\omega}$$
(8)

To complete the chemical reactivity characterization, the Electronic Fukui functions (f)(BULAT *et al.*, 2004) were computed from the electronic density of the computed FMO according to the equations 9 – 11 for the nucleophilic attack, electrophilic attack, and radical attack, respectively.(BETTENS *et al.*, 2020) The isosurfaces were obtained using the Multiwfn program(LU; CHEN, 2012) and rendered by the VESTA software.(MOMMA; IZUMI, 2011)

$$f^+ \approx \nu_{LUMO}$$
 (9)

$$f^- \approx \nu_{HOMO}$$
 (10)

$$f^0 \approx \frac{\rho_{HOMO} + \rho_{LUMO}}{2} \tag{11}$$

The Condensed Fukui functions (f_k) were determined using the Hirshfeld charge(HIRSHFELD, 1977) analysis obtained from the optimized geometry for each molecule for the nucleophilic attack $(f_k^+, \text{ equation 12})$, electrophilic attack $(f_k^-, \text{ equation 13})$, and radical attack $(f_k^0, \text{ equation 14})$. Also, the Δf index (equation 15) was computed for the SA1-A5 molecules. When the index is positive $(\Delta f > 0)$, the reactive site has nucleophilic character and a negative value for the index $(\Delta f < 0)$, it is associated with a reactive site which has a electrophilic character.(ALMEIDA-NETO *et al.*, 2020; MORELL; GRAND; TORO-LABBÉ, 2005; PAULA *et al.*, 2020)

$$f_k^+ = q_k(N+1) - q_k(N)$$
(12)

$$f_k^- = q_k(N) - q_k(N-1)$$
(13)

$$f_k^0 = \frac{q_k(N+1) - q_k(N-1)}{2}$$
(14)

$$\Delta f = f_k^+ - f_k^- \tag{15}$$

Where $q_k(N + 1)$, $q_k(N)$, and $q_k(N - 1)$ are the Hirshfeld charge in the atom k for the anionic, neutral, and cationic species. Finally, the Molecular Electrostatic Potential (MEP) was computed at the B3LYP/6-311+G (d, p) computational level for the title molecules. The isosurfaces for each electrostatic map were rendered by the Gabedit program.(ALLOUCHE, 2011)

2.2 Molecular Docking

The structure of cruzain receptor (PDB 1F29) was obtained from the Protein Data Bank, identified as "Crystal Structure Analysis of cruzain Bound to a Vinyl Sulfone Derived Inhibitor (I)", deposited at 2.15 Å resolution, determined by X-Ray Diffraction, classified as a hydrolase, in the organism Trypanosoma Cruzi and expressed in the Escherichia coli system.(BRINEN et al., 2000)

The enzyme preparation was performed by removing the H_2O molecules. The inhibitor derived from vinyl sulfone I (VS1) is present in the PDB file using the UCSF Chimera code,(PETTERSEN et al., 2004) thus eliminating the interference they could cause in the molecular docking result. Next step, the polar hydrogens were added to the protein structure using the Autodock Tools code with the residues removed.(MORRIS et al., 2009; SANNER, 1999) Then, ligand and enzyme were saved in PDBQT format for further reading in the software AutoDock Vina(ALLOUCHE, 2012) Docking simulations were performed using the AutoDock Vina code (version 1.1.2) with three-way multithreading.(ALLOUCHE, 2012) Docking simulations were performed using the AutoDock Vina code (version 1.1.2) with threeway multithreading.(BRINEN et al., 2000) The grid box was centered in protein with the parameters of 112Å x 58Å x 80Å and dimensions (x, y, z) = (11.514, -5.628, 11.363), and 100 independent simulations were performed, obtaining ten poses each. Data were obtained for comparison by performing simulations with the same parameters with benznidazole (BZN) (PubChem CID 31593), a nitroimidazole-derived drug with antiprotozoal activity, used for the treatment of Chagas disease41, with the natural inhibitor anacardic acid (AA) and with the vinyl sulfone I (VS1) derived inhibitor co-crystallized on the target enzyme. Discovery Studio Visualizer(DASSAULT SYSTÈMES BIOVIA, 2019) and UCSF Chimera(PETTERSEN et al., 2004) analyzed the results.

2.3 Molecular Dynamics simulation

The Gromacs (GROningen MAchine for Chemical Simulation) 2019.2 package *software*(BERENDSEN; VAN DER SPOEL; VAN DRUNEN, 1995) was used for performing all simulations by molecular dynamics (MD). CHARMM27(MACKERELL; BANAVALI; FOLOPPE, 2000) was the force field chosen for these simulations; ligands SA1, SA2, SA3, SA4, and SA5 were parameterized through SwissParam.(ZOETE *et al.*, 2011) Six triclinic boxes simulation was created for systems containing only protein 1F29 and 1F29-SA1, 1F29-

SA2, 1F29-SA3, 1F29-SA4, 1F29-SA5, 1F29-BZN complexes. Subsequently, 7360 water molecules described by the TIP3P model (JORGENSEN *et al.*, 1983), were additional, while for the neutralization of the system, 13 sodium ions were added.

The geometry of systems was optimized using two algorithms. The *steepest descent* (*ARFKEN; WEBER; HARRIS, 2013*) *is followed by the conjugate gradient (BORGIA; COYLE; ZWIERS, 2007*) with energy tolerance of 10 kJ mol⁻¹ nm⁻¹ and step size of 10⁻⁴ nm. Subsequently, two shorts 10 ns simulations were performed in each step equilibrium. The ensemble NVT used the V-rescale method(BUSSI; DONADIO; PARRINELLO, 2007) with a temperature of 310 K, while the ensemble NPT used the Parrinelo-Rahman barostat(PARRINELLO; RAHMAN, 1981) at a pressure of 1.0 bar. The production step MD was simulated in 200 ns through Leap-Frog integrator;(VAN GUNSTEREN; BERENDSEN, 1988) the same temperature and pressure used in the previous step were maintained. The server Protein-Ligand Interaction Profile (PLIP) (SALENTIN *et al.*, 2015) was utilized to analyze interactions of 1F29-SA1, 1F29-SA2, 1F29-SA3, 1F29-SA4, 1F29-SA5 and, 1F29-BZN complexes.

3 Results

3.1 Structural and spectroscopic analysis

The linear correlation between the calculated wavenumbers and the experimental wavenumbers of AA derivates, obtained from Reddy *et al*,(REDDY *et al.*, 2012) were made for each derivate. The results are shown in Fig.1. For the analysis of theoretical-experimental correlation, the coefficient of determination (R²) was computed. For the SA1-SA5 molecules (Fig. 2), the values of R² were found to be 0.9984 for the SA1, 0.9991 for the SA2, 0.9991 for the SA3, 0.9991 for the SA4, and 0.9994 for the SA5. These results indicate that the simulated molecules can describe with excellent agreement the experimental spectroscopic data. All the



scaled frequencies calculated have been detailed for each type of vibration in table S1.

Fig. 1. The linear correlation between the experimental wavenumbers and theoretical wavenumbers for the fundamental vibrational modes of the AA derivates molecules at the B3LYP/6-311+G (d, p) level of theory. (a) SA1; (b) SA2; (c) SA3; (d) SA4; (e) SA5.

The structure of the molecules SA1-SA5 (Fig. 2 and Fig. 3) was analyzed by performing a conformational scan of the dihedral angles of the most stable conformation. For scan calculations, the basis 6-31G (d, p) was used. The main scanning dihedral angles were Scan 1 C6-C1-C7-C8 (Fig. S1) // Scan 2 C22-C21-C20-S25 (Fig S2) // Scan 3 C5-C6-C9-O12 (Fig S3) //. The energy range shows the conformation of the minimum energy geometry of the

molecules. The energy varies up to 16 kcal.mol⁻¹, where the lowest local minima occur by the dihedral rotation of C1-C2-O7-C8 bonds.



Fig. 2. Structure 2D of the AA derivates molecules structured with the central A ring and the variations of derivatives on the R radical, highlighting the secondary aromatic B ring.

The initial, lowest energy point is the reference structure for comparison of the structures obtained from the conformations of the angular variation performed in 10 steps of 36° in each molecule and each scan Fig. S1-S3. The scans confirm the energy minimum used for the following calculations, besides observing points of energy minima.

The ¹³C NMR isotropic shielding was computed for the five derivates at the B3LYP/6-311+G(d, p) level of theory and GIAO(WOLINSKI; HINTON; PULAY, 1990) (gauge-independent atomic orbitals) method was used using Chloroform as an implicit solvent. The experimental values of the isotropic shielding were obtained from the work of Reddy *et al.* (REDDY *et al.*, 2012). The linear correlations between theoretical and the experimental values of the isotropic shielding are shown in Fig. 4. The coefficient of determination R² values was higher than 0.98, which implies an excellent agreement between the calculated molecule and the experimental data.



Fig. 3. Optimized geometries of the AA molecule and their derivatives SA1-SA5 for the B3LYP/6-311+G (d, p) level of theory.



Fig. 4. Linear correlation with the experimental ¹³C isotropic shielding and the calculated isotropic magnetic shielding at B3LYP/6–311+G (d, p) in Chloroform. (a) SA1; (b) SA2; (c) SA3; (d) SA4; (e) SA5.

3.2 Frontier Molecular Orbital and global quantum reactivity descriptors analysis

The Frontier Molecular Orbitals were computed at B3LYP/6-311+G(d,p) computational level and obtained from the SA1-SA5 optimized geometries (Fig 2), and the rendered isosurfaces are shown in Fig. 5. It can be seen that for all the five derivates, the HOMO is distributed mainly in the benzene ring and the methoxy group that is common for all the molecules. For the SA1 derivate, the LUMO is spread over mainly in the benzene ring and the ester group. For the other four derivates, the LUMO is spread over mainly in the benzene ring added to the sulfonamide group, as shown in Fig. 5. The chemical reactivity can be predicted

by the energy values of the HOMO and the LUMO since higher is the energy value of the HOMO orbital, higher is the susceptibility of the molecule to donate electronic density and lower is the energy of the LUMO orbital, higher is the susceptibility of the molecule to accept electronic density.(KOOPMANS, 1934) The energy values computed for the SA1-SA5 derivates are shown in Table 1, together with the values for those two molecular orbitals for the AA molecule. According to the data in Table 1 in respect to the HOMO energy value, the predicted order for the chemical reactivity is SA3 > SA4 > SA2 > SA5 > SA1 > AA. Hence, the chemical modifications on the AA molecule enhanced the chemical reactivity. The LUMO energy values predict the following order for the chemical reactivity: SA1 > AA > SA5 > SA4> SA3 > SA2. According to this result, only the SA1 derivate has an electrophilic character lower than the AA molecule. The Ionization potential (I) and the electron affinity (A) are related to the nucleophilic character and the electrophilic, respectively, and they are directly related to the HOMO and LUMO, respectively. Besides the HOMO and LUMO energy values, the energy gap (ΔE) between those two molecular orbitals is frequently used to measure chemical reactivity. According to the HOMO-LUMO energy gap data from the Table 1, the predicted order for the reactivity is SA2 > SA3 > SA4 > SA5 > AA > SA1. This result shows that SA2-5derivates are more reactive than the AA molecule, and only the SA1 exhibited less reactive than the precursor molecule.

The HOMO-LUMO energy gap is related to the concept of hard and soft molecules: the higher the energy gap, the higher is the hard character, and the lower the energy gap, the higher is the soft character of a molecule. Hence, the data obtained from the quantum descriptors global hardness (η) and global softness (σ) show that the predicted order for the chemical reactivity is the same as the energy gap.

Electronegativity corresponds to the tendency to attract electronic density, where a high value indicates a strong electronic attraction. Thus, the value of SA2 was the highest identified, followed by the sequence in descending order: AA > SA4 > SA3 > SA5 > SA1.

Finally, the quantum descriptors electrophilicity index (ω) and nucleophilicity index (ε) are related to the electrophilic and nucleophilic character, respectively. The order predicted by the electrophilicity index is SA2 > SA3 > SA4 > AA > SA5 > SA1. The order predicted by the nucleophilicity index is SA1 > SA5 > AA > SA4 > SA3 > SA2, which is the opposite from the obtained from the electrophilicity index. Therefore, the chemical reactivity of these derivates is ruled by the electrophilic character of the molecule, hence the SA2

molecule should be the most reactive molecule when compared to the other derivates and the AA molecule.



Fig. 5. Frontier Molecular Orbitals (HOMO and LUMO) and the energy gap (ΔE) calculated for the AA and Derivates (SA1-5) at B3LYP/6–311+G (d, p) level of theory.

3.4 Local quantum reactivity descriptors

The reactivity at a specific molecule site can be described by the Fukui functions (Electronic and Condensed) analysis and the Δf index (local reactivity descriptors).(MORELL; GRAND; TORO-LABBÉ, 2005) The results of the isosurfaces of 0.03 from the electronic Fukui functions for the nucleophilic attack (f_k^+) and electrophilic attack (f_k^-) are shown in Fig. 6 for the five derivates of the AA molecule. It was common for all the five molecules that the regions with tendency for a nucleophilic and electrophilic attacks were, respectively, the ester group and the benzene ring since the ester group has higher electronic density spread over this

group which can be used to donate electronic density and the benzene ring has empty molecular orbitals that can be used to accept the electronic density and this negative charged is delocalized due to the resonance effect. Also, the Condensed Fukui functions and the Δf index were computed using the Hirshfeld charge population analysis for the nucleophilic attack (f_k^+) and electrophilic attack (f_k^-).(LIU; RONG; LU, 2014; OLÁH; ALSENOY; SANNIGRAHI, 2002; ROY, 2003) The results for the SA1-A5 derivates are shown in Tables S1 - S5 in the Supplementary Material. According to these results, for the SA1 molecule, the atoms that are more susceptible for a nucleophilic attack are C3, C5, C8, C9, O10, C11, O12, C17, C18, C19, C20 and the atoms more susceptible for an electrophilic attack are C1, C2, C4, C6, O7, C13, C14, C15, C16 N21, S22, O23, O24, and C25; for the SA2 molecule, the atoms that are more susceptible for a nucleophilic attack are C3, C5, C8, C9, O10, C11, and O12 and the atoms more susceptible for an electrophilic attack are C1, C2, C4, C6, O7, C13, C14, C15, C16, C17, C18, C19, C20, N21, S22, O23, O24, C25, C26, C27, C28, C29, and C30; for the SA3 molecule, the atoms that are more susceptible for a nucleophilic attack are C3, C5, C8, C9, O10, C11, O12, C18, C19, C20, S22, O23, C25, C26, C27, C28, C29, C30, and C31 and the atoms more susceptible for an electrophilic attack are C1, C2, C4, C6, C7, C13, C14, C15, C16, C17, N21, and O24; for the SA4 molecule, the atoms that are more susceptible for a nucleophilic attack are C3, C5, C8, C9, O10, C11, O12, C13, C15, C17, C18, C19, C20, S22, C25, C26, C27, C28, C29, C30, and C31 and the atoms more susceptible for an electrophilic attack are C1, C2, C4, C6, O7, C14, C16, N21, O23, and O24; for the SA5 molecule, the atoms that are more susceptible for a nucleophilic attack are C3, C5, C8, C9, O10, C11, O12, C18, C19, C20, N21, S22, C25, C26, C27, C28, C29, C30, C31, and C32 and the atoms more susceptible for an electrophilic attack are C1, C2, C4, C6, O7, C13, C14, C15, C16, C17, O23, and O24.



Fig. 6. Calculated isosurfaces for the Electronic Fukui functions using the electronic density and computed at B3LYP/6-311+G (d, p) computational level.

3.5 Molecular Electrostatic Potential (MEP)

The Molecular Electrostatic Potential (MEP) was determined for the SA1-SA5 molecules, and the rendered isosurfaces are shown in Fig. 7. It can be seen from Fig. 7 a color variation from red to blue. The order of color trend red \rightarrow orange \rightarrow yellow \rightarrow green \rightarrow blue represents the tendency of nucleophilicity to electrophilicity on a scale of -0.05 eV to 0.05 eV, respectively. The regions of the MEP with greater localized electronic density (negatively charged region) will tend to be red, which is associated with a nucleophilic character. The regions with less localized electronic density (positively charged) will be blue, related to an electrophilic character. Fig. 7 shows that the ester group and the oxygen atom from the sulfonamide group have a higher electronic density concentration, indicating that it is favorable to donate the electronic density (nucleophilic character). While the methoxy group, methyl (SA1), and phenyl (SA2-SA5) of the sulfonamide are regions with low electrophilic character). This result is directly related to the Electronic Fukui functions: the red-colored regions in the MEP of the SA1-5 indicate a negative charge that can donate a nucleophilic attack, and the
benzene ring can accept extra electronic density since the negative charge is distributed over the entire aromatic ring as shown in the MEP in Fig. 7.



Fig. 7. Calculated Molecular Electrostatic Potential (MEP) at B3LYP/6-311+G(d,p) level of theory for the SA1- SA5 molecules.

3.6 Molecular Docking

Molecular docking simulations were performed with the cruzain receptor to investigate the potential in silico antichagasic effect of the anacardic acid-derived ligands (SA1, SA2, SA3, SA4 and SA5). All the analyzed ligands showed RMSD (Root Mean Square Deviation) values within the ideal parameter, less than 2.0 Å,(YUSUF *et al.*, 2008) in the order of 1.885 Å (SA1), 1. 748 Å (SA2), 1.219 Å (SA3), 1.435 Å (SA4), 1.740 Å (SA5), 1.709 Å (AA), 1.700 Å (BZN) and 1.658 Å (VS1 redocking) indicating the statistical validation of the simulations. In addition, affinity energy was used as a criterion to evaluate the protein/ligand complexes formed, being considered ideal values, those below -6.0 kcal/mol.(SHITYAKOV; FÖRSTER, 2014) . The ligands evaluated showed affinity energy with the cruzain receptor in the order of -4.2 kcal.mol⁻¹ (SA1), -4.5 kcal.mol⁻¹ (SA2), -3.9 kcal.mol⁻¹ (SA3), -4.9 kcal.mol⁻¹

¹ (SA4), -4.8 kcal/mol (SA5), -3.9 kcal/mol (AA), -5.0 kcal/mol (BZN) and -7.2 kcal/mol (VS1 redocking). It can be pointed out that the affinity values of the SA1, SA2, SA4, and SA5 derivatives were better than the anacardic acid (AA). The coupling of the ligands can be observed in Fig. 8.



Fig. 8: Interaction complex of the receptor cruzain with ligands VS1 (a), BZN (b), SA1 (c), SA2 (d), SA3 (e), SA4 (f), SA5(g), AA (h).

Table 2 shows the binding distances between the amino acid residues of the enzyme and the ligand molecules, in which it was possible to observe that the ligands SA1, SA2, and

AA were close to the binding site of BZN and VS1 (inhibitor co-crystallized in the enzyme PDB), and therefore close to the active site, it was also observed that in the redocking the co-crystallized inhibitor docked in the same region of cruzain, validating the docking simulations performed.

SA1 and SA2 performed better and closer to the site residues (His159, Cys25, Asn175, Gln19, and Trp177). SA3, SA4, and SA5 showed higher values than the reference values (BZN and VS1 PDB), which may be related to the presence of methylation in the structures' phenyl radical, SA3 ortho-methylated, SA4 para-methylated, and SA5 ortho-methylated.

			0		1			0	
Residue	SA1	SA2	SA3	SA4	SA5	ΑΑ	BZN	VS1 PDB	VSI
Ttostaac	5111	0112	5110	5111			221	Native	Redocking
His159	3.1	3.7	16.0	6.9	15.3	7.1	3.1	3.1	3.4
Cys 25	3.7	3.5	15.6	7.9	10.8	8.0	4.3	2.6	3.7
Asn 175	6.7	7.0	8.2	6.8	18.6	6.8	6.5	6.8	6.9
Gln 19	3.1	3.0	13.5	4.9	11.4	3.7	3.3	3.2	3.0
Trp 177	3.6	3.5	10.9	3.5	15.8	3.4	2.6	3.2	3.9

 Table 2. Binding residue/protein distances in angstroms

From the analysis of molecular interactions (Fig. 9.), it was observed that the ligands SA2 and BZN presented two interactions with the residue of the active site of the enzyme Cys25, being a Conventional Hydrogen Bond with SA2 and a Hydrophobic interaction with BZN. The interactions were also observed with Trp177, a highly conserved residue in the enzyme, presenting π - π Stacked interactions with the ligands SA1, SA2, SA4, AA, and BZN. The Amide-Pi Stacked interaction with SA2 and Hydrophobic interaction with SA4 (table S7). The ligands SA3 and SA5 are docked in different regions. Thus no interactions with the residues of the cruzain active site were observed. For the SA1, SA2, and SA4 compounds, the interaction between the amino acid Trp177 with the benzene ring of these molecules is a π - π stacked type since this group is more susceptible to accept electronic density predicted by the Electronic Fukui functions.



Fig. 9: SA1 (A), SA2 (B), SA3 (C), SA4 (D), SA5 (E), AA (F) and BZN (G) molecular interactions with cruzain.

3.7 Molecular Dynamics Analysis

The root mean square deviation (RMSD) is used to analyze whether the system has reached equilibrium. Fig. 10 showed similar values RMSD for the protein 1F29 and for the 1F29-SA1, 1F29-SA2, 1F29-SA3, 1F29-SA4, 1F29-SA5 complexes. The protein and the complexes cited above reached equilibrium at the beginning of MD simulations. The 1F29-BZN complex showed the highest values RMSD and reached the equilibrium from 50 ns. Therefore, the ligand BZN had fewer stable interactions with the protein 1F29 concerning the

other ligands (SA1, SA2, SA3, SA4, and SA5). The following analyzes will be carried out only in the equilibrium time interval previously recorded.



Fig. 10: Determination of root mean square deviation (RMSD) of unbounded 1F29 (black) and 1F29-SA1 (red), 1F29-SA2 (green), 1F29-SA3 (blue), 1F29-SA4 (yellow), 1F29-SA5 (brown), and 1F29-BZN (cyan) complexes.

The Coulomb and Lennard-Jones short-range energies were calculated and have been added between receptor 1F29 with SA1, SA2, SA3, SA4, SA5, and BZN ligands, shown in Fig. 11. 1F29-SA1, 1F29-SA2, 1F29-SA3, and 1F29-SA5 complexes showed similar interaction energies, in the value of -130.913 kJ mol⁻¹ (63.314), -102.607 kJ mol⁻¹ (52.214), -108.907 kJ mol⁻¹ (55.580), -101.549 kJ mol⁻¹(56.744), respectively. When compared to the interaction energies of the above complexes, the 1F29-SA4 complex has the highest interaction energy of -179.217 kJ mol⁻¹ (85.031), while that the 1F29-BZN has the smaller interaction energy in the value of -26.151 kJ mol⁻¹ (18.105).



Fig. 11: Energies of interaction present in the 1F29-SA1, 1F29-SA2, 1F29-SA3, 1F29-SA4, 1F29-SA5, and 1F29-BZN complexes, with standard deviation.

The Fig. 12 shows the main interactions calculated between complexes analyzed in its last simulation frame (200 ns). SA1 ligand presented two hydrogen bonds with Gln 180 and Gly 182 amino acids, with distance 1.65 Å and 3.13 Å, respectively (Fig. 12a); moreover, two hydrophobic interactions occurred between Trp 177 and Met 142 with SA1 ligand, with values of 3.84 Å and 3.69 Å, respectively. His 159 shows a charge center with SA1, with a distance of 4.67 Å. 1F29-SA3 (Fig. 12c) and 1F29-SA5 (Fig. 12e) complexes show only hydrophobic interactions. The first one with Ala 122 (3.52 Å) and Trp 123 (3.92 Å); and second one with Trp 123 (3.93 Å), Val 126 (3.87 Å). The 1F29-SA2 complex interacts hydrophobically with Val 126 and Ala 122 amino acids residues, with a distance of 3.70 Å and 3.74 Å, respectively (Fig. 12b). Moreover, the ligand SA2 showed a hydrogen bond with Asn 127, with a distance of 1.93 Å. The BZN ligand (Fig. 12f) interacts hydrophobically with the Ala 1 (3.50 Å), Ala 121 (3.69 Å), Tyr 166 (4.00 Å) amino acids. Besides, was registered a charge center with the Lys 191 (5.59 Å) amino acid and one hydrogen bond with the Ala 1 (2.29 Å) amino acid. Between 1F29 and SA4 (Fig. 12d), there are three hydrophobic interactions with Trp 177 and His 159 (distance of 3.74 Å, 3.75 Å, and 3.94 Å, respectively); Moreover, two hydrogen bonds uncharged of moderate strength were registered with the amino acids Gln 19 (1.82 Å), His 159

(2.05 Å), and a weak one with Trp 177 (2.50 Å). These bonds are responsible for the high interaction energy observed for this complex concerning the others (1F29-SA1, 1F29-SA2, 1F29-SA3, and 1F29-SA5), this intermolecular force contributes from 11 to 60 kJ mol⁻¹ in the interaction energy(ELEMANS; LEI; DE FEYTER, 2009). Besides, this intermolecular force is the strongest and most influential in molecular recognition (DONG; DAVIS, 2021).



Fig. 12: Interactions presents in the (a) 1F29-SA1, (b) 1F29-SA2, (c) 1F29-SA3, (d) 1F29-SA4, (e) 1F29-SA5, and (f) 1F29-BZN complexes.

Conclusions

Quantum chemical calculations using the DFT method at the B3LYP/6-311+G (d, p) level were performed to compare with the experimental and theoretical spectroscopic data measured in NMR and IR. It was verified that the calculated structural data showed an excellent concordance with those experimental ones. The reactivity analysis observed that modification of the anacardic acid (AA) to the SA1-SA5 derivatives improved the overall reactivity. In molecular docking, it was indicated that the SA1, SA2, and SA4 molecules performed better in their interactions with the cruzain. They maintain an excellent interaction with the residues of the enzyme, indicating that the chemical substitutions made to the AA favor the interaction with the cruzain. The results of molecular dynamics indicate that the SA4 ligand showed high interaction energy with the 1F29 protein due to two moderate and one weak hydrogen bond uncharged in this complex. Thus, we can conclude that the anacardic acid derivatives could be promised as drugs for treating Chagas disease.

Conflicts of interest

There are no conflicts to declare.

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Supplementary Material



Fig S1. Scan atoms : C6-C1-C7-C8



Fig S2. Scan atoms :: C22-C21-C20-S25



Fig S3. Scan atoms: C5-C6-C9-O12

Vibrational mode	SA1	SA2	SA3	SA4	SA5
Stretch N-H	3417.63	3408.47	3420.11	3405.52	3399.61
Bending C-N-H	1267.148 1332.401	1308.619	1269.816	1333.717	1071.618
Bending C-C-H	1156.16 1104.9 1267.148 1581.211 1568.575	1581.26 1105.825 853.0441	3061.736 1156.488 1105.287	1269.893 1156.861 1105.94 1066.188	1264.677 1156.616 962.8653
Stretch C-C ring benzenic	1581.211 1568.575	1581.26		813.5692	
Stretch C-H : metyl of ester	3021.024	3021.378		3054.329	
Bending C-H metyl of ester	968.0704 1435.705 1713.819	1714.372	1714.582 1156.488 754.3548	1714.545 1435.539 1156.861 1105.94 1066.188	1713.824 1264.677 1156.616 1105.64
Stretch H-C-H : aliphatic chain	2934.84 2895.308	2928.559 2895.612	2933.687 2894.5	2896.271	2928.766 2894.394
Bending C-C-H : aliphatic chain	1465.37 1332.401	1459.335 1308.619 1269.816 1105.825	1467.132 1307.943 1266.638 1105.287 754.3548	1467.494 1333.717 1269.893 1105.94 1066.188	1465.883 1323.172 1105.64 1071.618
Stretch C -C aliphatic chain	968.0704	1081.633	997.3531		962.8653
Bending C-C-C of aliphatic chain	823.1653 1067.955		1074.108		
Stretch C - O ether		1105.825	1105.287	1066.188	

Table S1. Scaled frequencies calculated for each type of vibration

Stretch C=O ester	1713.819	1714.372	1714.582	1714.545	1713.824
				813.5692	
Stretch S=O sulfonamide	1067.955		1074.108		1071.618
Stretch N-S	823.1653				
Stretch C-N			965.3381		
Stretch C-H ring benzenic (B)		3067.761			
Bending C-C-H ring benzenic (B)		1459.335 1159.965	1581.858 1266.638 754.3548	1584.804	1264.677 1594.059 1071.618 899.0091
Stretch C-C ring benzenic (B)			1581.858	1584.804	1264.677 1594.059
Stretch C-H metyl ring benzenic (B)			3061.736	2930.128	3017.77
Bendind C-C-H metyl ring benzenic (B)			1432.124 1074.108		1432.708 1264.677 899.0091

Table S2. Condensed Fukui functions calculated by the Hirshfeld charge population for the SA1

Atom	$f^{\scriptscriptstyle +}$	f	f^{\bullet}	Δf
1(C)	0.021598	0.06717	0.044384	-0.04557
2(C)	0.041137	0.065634	0.053386	-0.0245
3(C)	0.067449	0.052959	0.060204	0.01449
4(C)	0.029404	0.108969	0.069187	-0.07957
5(C)	0.037854	0.033058	0.035456	0.004796
6(C)	0.038625	0.04452	0.041573	-0.0059
7(O)	0.011843	0.096438	0.054141	-0.0846
8(C)	0.038253	0.025639	0.031946	0.012614
9(C)	0.041526	0.002986	0.022256	0.03854
10(O)	0.019997	0.006634	0.013316	0.013363

11(C)	0.021533	0.011692	0.016613	0.009841
12(O)	0.055092	0.040448	0.04777	0.014644
13(C)	0.00663	0.007879	0.007255	-0.00125
14(C)	0.004882	0.006261	0.005572	-0.00138
15(C)	0.004179	0.005659	0.004919	-0.00148
16(C)	0.002831	0.003633	0.003232	-0.0008
17(C)	0.004532	0.003791	0.004162	0.000741
18(C)	0.003713	0.002896	0.003305	0.000817
19(C)	0.00549	0.003112	0.004301	0.002378
20(C)	0.003856	0.002685	0.003271	0.001171
21(N)	3.7E-05	0.003586	0.001812	-0.00355
22(S)	0.007033	0.012308	0.009671	-0.00527
23(O)	0.008677	0.02911	0.018894	-0.02043
24(O)	0.005764	0.025559	0.015662	-0.0198
25(C)	0.003991	0.006742	0.005367	-0.00275
26(H)	0.053076	0.033011	0.043044	0.020065
27(H)	0.051267	0.035568	0.043418	0.015699
28(H)	0.026042	0.042979	0.034511	-0.01694
29(H)	0.050759	0.027326	0.039043	0.023433
30(H)	0.040424	0.027148	0.033786	0.013276
31(H)	0.056618	0.027168	0.041893	0.02945
32(H)	0.019198	0.012219	0.015709	0.006979
33(H)	0.025506	0.013582	0.019544	0.011924
34(H)	0.020095	0.009771	0.014933	0.010324
35(H)	0.008868	0.014123	0.011496	-0.00526
36(H)	0.016605	0.015438	0.016022	0.001167
37(H)	0.008618	0.004769	0.006694	0.003849
38(H)	0.002857	0.004451	0.003654	-0.00159
39(H)	0.006781	0.006469	0.006625	0.000312
40(H)	0.008202	0.00719	0.007696	0.001012
41(H)	0.00698	0.003621	0.005301	0.003359
42(H)	0.003735	0.003013	0.003374	0.000722
43(H)	0.006593	0.004142	0.005368	0.002451
44(H)	0.01371	0.003765	0.008738	0.009945
45(H)	0.010118	0.002684	0.006401	0.007434
46(H)	0.00591	0.00246	0.004185	0.00345
47(H)	0.020956	0.003152	0.012054	0.017804
48(H)	0.007257	0.003149	0.005203	0.004108
49(H)	0.013328	0.002425	0.007877	0.010903
50(H)	0.00451	0.002329	0.00342	0.002181
51(H)	0.00459	0.003606	0.004098	0.000984

52(H)	0.005356	0.005661	0.005509	-0.00031
53(H)	0.008199	0.006286	0.007243	0.001913
54(H)	0.002159	0.002984	0.002572	-0.00082

Table S3. Condensed Fukui functions calculated by the Hirshfeld charge population for the SA2

Atom	$f^{\scriptscriptstyle +}$	f	f•	Δf
1(C)	0.022787	0.065793	0.04429	-0.04301
2(C)	0.042978	0.064484	0.053731	-0.02151
3(C)	0.075476	0.051838	0.063657	0.023638
4(C)	0.033255	0.106807	0.070031	-0.07355
5(C)	0.041891	0.032372	0.037132	0.009519
6(C)	0.042661	0.04343	0.043046	-0.00077
7(O)	0.009897	0.094306	0.052102	-0.08441
8(C)	0.035165	0.025113	0.030139	0.010052
9(C)	0.037851	0.002848	0.02035	0.035003
10(O)	0.017583	0.006555	0.012069	0.011028
11(C)	0.044694	0.011454	0.028074	0.03324
12(O)	0.054758	0.039397	0.047078	0.015361
13(C)	0.006799	0.007807	0.007303	-0.00101
14(C)	0.004769	0.006224	0.005497	-0.00146
15(C)	0.003913	0.005775	0.004844	-0.00186
16(C)	0.002324	0.003854	0.003089	-0.00153
17(C)	0.002449	0.004107	0.003278	-0.00166
18(C)	0.001325	0.003298	0.002312	-0.00197
19(C)	0.001112	0.003637	0.002375	-0.00252
20(C)	0.00087	0.003209	0.00204	-0.00234
21(N)	-0.00045	0.004199	0.001873	-0.00465
22(S)	0.001809	0.011975	0.006892	-0.01017
23(O)	0.001394	0.022662	0.012028	-0.02127
24(O)	0.004894	0.031368	0.018131	-0.02647
25(C)	-0.00087	-0.00034	-0.0006	-0.00053
26(C)	0.000349	0.001606	0.000978	-0.00126
27(C)	-7.8E-05	0.001167	0.000545	-0.00125
28(C)	0.001701	0.004393	0.003047	-0.00269
29(C)	0.002225	0.005238	0.003732	-0.00301
30(C)	0.002897	0.006647	0.004772	-0.00375
31(H)	0.031432	0.032437	0.031935	-0.00101
32(H)	0.046266	0.034905	0.040586	0.011361
33(H)	0.027096	0.042181	0.034639	-0.01509

$\begin{array}{llllllllllllllllllllllllllllllllllll$	34(H)	0.074081	0.02679	0.050436	0.047291
36(H) 0.042639 0.026604 0.034622 0.016035 37(H) 0.050465 0.009553 0.030009 0.040912 38(H) 0.072583 0.013347 0.042965 0.059236 39(H) 0.03859 0.011905 0.025248 0.026685 40(H) 0.016289 0.015126 0.015708 0.001163 41(H) 0.002437 0.004208 0.003323 -0.00177 43(H) 0.007368 0.004895 0.006132 0.00224 45(H) 0.007281 0.0073 0.007291 -1.9E-05 46(H) 0.002954 0.002981 0.002968 -2.7E-05 47(H) 0.004485 0.004323 -7.5E-05 48(H) 0.004285 0.00436 0.004323 -7.5E-05 49(H) 0.004344 0.00322 0.00066 51(H) 0.001254 0.00217 -0.0011 52(H) 0.001254 0.00217 -0.00116 52(H) -0.00138 53(H) 0.002232 0.00333	35(H)	0.028301	0.02658	0.027441	0.001721
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	36(H)	0.042639	0.026604	0.034622	0.016035
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	37(H)	0.050465	0.009553	0.030009	0.040912
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	38(H)	0.072583	0.013347	0.042965	0.059236
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	39(H)	0.03859	0.011905	0.025248	0.026685
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	40(H)	0.016289	0.015126	0.015708	0.001163
42(H) 0.002437 0.004208 0.003323 -0.00177 $43(H)$ 0.007368 0.004895 0.006132 0.002473 $44(H)$ 0.00657 0.006346 0.006458 0.000224 $45(H)$ 0.007281 0.0073 0.007291 $-1.9E-05$ $46(H)$ 0.002954 0.002981 0.002968 $-2.7E-05$ $47(H)$ 0.004144 0.003819 0.003982 0.000325 $48(H)$ 0.004285 0.00436 0.004323 $-7.5E-05$ $49(H)$ 0.004344 0.00382 0.004082 0.000524 $50(H)$ 0.002271 0.002928 0.0026 -0.00066 $51(H)$ 0.001254 0.00311 0.002182 -0.00111 $52(H)$ 0.001254 0.00353 0.002881 -0.0013 $54(H)$ 0.001827 0.00259 0.002209 -0.00076 $55(H)$ 0.00144 0.002415 0.001428 -0.00198 $56(H)$ 0.001197 0.001349 0.002271 -0.00216 $57(H)$ 0.001197 0.001348 0.00347 -0.00171 $58(H)$ 0.002851 0.004088 0.00347 -0.00124 $60(H)$ 0.00319 0.004671 0.003931 -0.00148 $61(H)$ 0.003591 0.005083 0.004337 -0.00149	41(H)	0.008254	0.013886	0.01107	-0.00563
43(H) 0.007368 0.004895 0.006132 0.002473 $44(H)$ 0.00657 0.006346 0.006458 0.000224 $45(H)$ 0.007281 0.0073 0.007291 $-1.9E-05$ $46(H)$ 0.002954 0.002981 0.002968 $-2.7E-05$ $47(H)$ 0.004144 0.003819 0.003982 0.000325 $48(H)$ 0.004285 0.00436 0.004323 $-7.5E-05$ $49(H)$ 0.004344 0.00382 0.004082 0.000524 $50(H)$ 0.002271 0.002928 0.0026 -0.00066 $51(H)$ 0.001254 0.00311 0.002182 -0.00116 $52(H)$ 0.001254 0.00311 0.002182 -0.00186 $53(H)$ 0.00232 0.00259 0.002209 -0.00076 $55(H)$ 0.00144 0.002415 0.001428 -0.00198 $56(H)$ 0.001192 0.003349 0.002271 -0.00216 $57(H)$ 0.001197 0.0013349 0.002271 -0.00216 $57(H)$ 0.00157 0.001348 0.00347 -0.00171 $58(H)$ 0.002851 0.004088 0.00347 -0.00148 $61(H)$ 0.003591 0.005083 0.004337 -0.00149	42(H)	0.002437	0.004208	0.003323	-0.00177
44(H)0.006570.0063460.0064580.00022445(H)0.0072810.00730.007291-1.9E-0546(H)0.0029540.0029810.002968-2.7E-0547(H)0.0041440.0038190.0039820.00032548(H)0.0042850.004360.004323-7.5E-0549(H)0.0043440.003820.0040820.00052450(H)0.0022710.0029280.0026-0.0006651(H)0.0012540.003110.002182-0.0018653(H)0.0022320.003530.002881-0.001354(H)0.0018270.002590.002209-0.0007655(H)0.0011920.0033490.002271-0.0021657(H)0.0011970.0019020.00155-0.0007158(H)0.000570.0013480.000347-0.0012460(H)0.003190.0046710.003931-0.0014861(H)0.0035910.0050830.004337-0.00149	43(H)	0.007368	0.004895	0.006132	0.002473
45(H) 0.007281 0.0073 0.007291 $-1.9E-05$ $46(H)$ 0.002954 0.002981 0.002968 $-2.7E-05$ $47(H)$ 0.004144 0.003819 0.003982 0.000325 $48(H)$ 0.004285 0.00436 0.004323 $-7.5E-05$ $49(H)$ 0.004344 0.00382 0.004082 0.000524 $50(H)$ 0.002271 0.002928 0.0026 -0.00066 $51(H)$ 0.001254 0.00311 0.002182 -0.00186 $53(H)$ 0.002232 0.00353 0.002881 -0.0013 $54(H)$ 0.001827 0.00259 0.002209 -0.00076 $55(H)$ 0.00144 0.002415 0.001428 -0.00198 $56(H)$ 0.001192 0.003349 0.002271 -0.00216 $57(H)$ 0.00057 0.001348 0.000959 -0.00078 $59(H)$ 0.002851 0.004671 0.003931 -0.00148 $61(H)$ 0.003591 0.005083 0.004337 -0.00149	44(H)	0.00657	0.006346	0.006458	0.000224
46(H) 0.002954 0.002981 0.002968 $-2.7E-05$ $47(H)$ 0.004144 0.003819 0.003982 0.000325 $48(H)$ 0.004285 0.00436 0.004323 $-7.5E-05$ $49(H)$ 0.004344 0.00382 0.004082 0.000524 $50(H)$ 0.002271 0.002928 0.0026 -0.00066 $51(H)$ 0.001254 0.002567 0.002017 -0.0011 $52(H)$ 0.001254 0.00311 0.002182 -0.00186 $53(H)$ 0.002232 0.00353 0.002881 -0.0013 $54(H)$ 0.001827 0.00259 0.002209 -0.00076 $55(H)$ 0.00144 0.002415 0.001428 -0.00198 $56(H)$ 0.001192 0.003349 0.002271 -0.00216 $57(H)$ 0.00057 0.001348 0.000959 -0.00078 $59(H)$ 0.002851 0.004671 0.003931 -0.00148 $61(H)$ 0.003591 0.005083 0.004337 -0.00149	45(H)	0.007281	0.0073	0.007291	-1.9E-05
47(H)0.0041440.0038190.0039820.00032548(H)0.0042850.004360.004323-7.5E-0549(H)0.0043440.003820.0040820.00052450(H)0.0022710.0029280.0026-0.0006651(H)0.0014660.0025670.002017-0.001152(H)0.0012540.003110.002182-0.0018653(H)0.0022320.003530.002881-0.001354(H)0.0018270.002590.002209-0.0007655(H)0.001420.0033490.002271-0.0021657(H)0.0011920.0033490.002271-0.0021657(H)0.001970.0013480.000959-0.0007858(H)0.000570.0013480.00347-0.0012460(H)0.003190.0046710.003931-0.0014861(H)0.0035910.0050830.004337-0.00149	46(H)	0.002954	0.002981	0.002968	-2.7E-05
48(H)0.0042850.004360.004323-7.5E-0549(H)0.0043440.003820.0040820.00052450(H)0.0022710.0029280.0026-0.0006651(H)0.0014660.0025670.002017-0.001152(H)0.0012540.003110.002182-0.0018653(H)0.0022320.003530.002881-0.001354(H)0.0018270.002590.002209-0.0007655(H)0.000440.0024150.001428-0.0019856(H)0.0011920.0033490.002271-0.0021657(H)0.0011970.0019020.00155-0.0007158(H)0.000570.0013480.000959-0.0007859(H)0.0028510.0040880.00347-0.0012460(H)0.003190.0046710.003931-0.0014861(H)0.0035910.0050830.004337-0.00149	47(H)	0.004144	0.003819	0.003982	0.000325
49(H)0.0043440.003820.0040820.00052450(H)0.0022710.0029280.0026-0.0006651(H)0.0014660.0025670.002017-0.001152(H)0.0012540.003110.002182-0.0018653(H)0.0022320.003530.002881-0.001354(H)0.0018270.002590.002209-0.0007655(H)0.000440.0024150.001428-0.0019856(H)0.0011920.0033490.002271-0.0021657(H)0.0011970.0019020.00155-0.0007158(H)0.000570.0013480.000347-0.0012460(H)0.003190.0046710.003931-0.0014861(H)0.0035910.0050830.004337-0.00149	48(H)	0.004285	0.00436	0.004323	-7.5E-05
50(H)0.0022710.0029280.0026-0.0006651(H)0.0014660.0025670.002017-0.001152(H)0.0012540.003110.002182-0.0018653(H)0.0022320.003530.002881-0.001354(H)0.0018270.002590.002209-0.0007655(H)0.000440.0024150.001428-0.0019856(H)0.0011920.0033490.002271-0.0021657(H)0.0011970.0019020.00155-0.0007158(H)0.000570.0013480.00347-0.0012460(H)0.003190.0046710.003931-0.0014861(H)0.0035910.0050830.004337-0.00149	49(H)	0.004344	0.00382	0.004082	0.000524
51(H)0.0014660.0025670.002017-0.001152(H)0.0012540.003110.002182-0.0018653(H)0.0022320.003530.002881-0.001354(H)0.0018270.002590.002209-0.0007655(H)0.000440.0024150.001428-0.0019856(H)0.0011920.0033490.002271-0.0021657(H)0.0011970.0019020.00155-0.0007158(H)0.000570.0013480.000959-0.0007859(H)0.0028510.0040880.00347-0.0012460(H)0.003190.0046710.003931-0.0014861(H)0.0035910.0050830.004337-0.00149	50(H)	0.002271	0.002928	0.0026	-0.00066
52(H)0.0012540.003110.002182-0.0018653(H)0.0022320.003530.002881-0.001354(H)0.0018270.002590.002209-0.0007655(H)0.000440.0024150.001428-0.0019856(H)0.0011920.0033490.002271-0.0021657(H)0.0011970.0019020.00155-0.0007158(H)0.000570.0013480.000959-0.0007859(H)0.0028510.0040880.00347-0.0012460(H)0.003190.0050830.004337-0.00149	51(H)	0.001466	0.002567	0.002017	-0.0011
53(H)0.0022320.003530.002881-0.001354(H)0.0018270.002590.002209-0.0007655(H)0.000440.0024150.001428-0.0019856(H)0.0011920.0033490.002271-0.0021657(H)0.0011970.0019020.00155-0.0007158(H)0.000570.0013480.000959-0.0007859(H)0.0028510.0040880.00347-0.0012460(H)0.003190.0046710.003931-0.0014861(H)0.0035910.0050830.004337-0.00149	52(H)	0.001254	0.00311	0.002182	-0.00186
54(H)0.0018270.002590.002209-0.0007655(H)0.000440.0024150.001428-0.0019856(H)0.0011920.0033490.002271-0.0021657(H)0.0011970.0019020.00155-0.0007158(H)0.000570.0013480.000959-0.0007859(H)0.0028510.0040880.00347-0.0012460(H)0.003190.0046710.003931-0.0014861(H)0.0035910.0050830.004337-0.00149	53(H)	0.002232	0.00353	0.002881	-0.0013
55(H)0.000440.0024150.001428-0.0019856(H)0.0011920.0033490.002271-0.0021657(H)0.0011970.0019020.00155-0.0007158(H)0.000570.0013480.000959-0.0007859(H)0.0028510.0040880.00347-0.0012460(H)0.003190.0046710.003931-0.0014861(H)0.0035910.0050830.004337-0.00149	54(H)	0.001827	0.00259	0.002209	-0.00076
56(H)0.0011920.0033490.002271-0.0021657(H)0.0011970.0019020.00155-0.0007158(H)0.000570.0013480.000959-0.0007859(H)0.0028510.0040880.00347-0.0012460(H)0.003190.0046710.003931-0.0014861(H)0.0035910.0050830.004337-0.00149	55(H)	0.00044	0.002415	0.001428	-0.00198
57(H)0.0011970.0019020.00155-0.0007158(H)0.000570.0013480.000959-0.0007859(H)0.0028510.0040880.00347-0.0012460(H)0.003190.0046710.003931-0.0014861(H)0.0035910.0050830.004337-0.00149	56(H)	0.001192	0.003349	0.002271	-0.00216
58(H)0.000570.0013480.000959-0.0007859(H)0.0028510.0040880.00347-0.0012460(H)0.003190.0046710.003931-0.0014861(H)0.0035910.0050830.004337-0.00149	57(H)	0.001197	0.001902	0.00155	-0.00071
59(H)0.0028510.0040880.00347-0.0012460(H)0.003190.0046710.003931-0.0014861(H)0.0035910.0050830.004337-0.00149	58(H)	0.00057	0.001348	0.000959	-0.00078
60(H)0.003190.0046710.003931-0.0014861(H)0.0035910.0050830.004337-0.00149	59(H)	0.002851	0.004088	0.00347	-0.00124
61(H) 0.003591 0.005083 0.004337 -0.00149	60(H)	0.00319	0.004671	0.003931	-0.00148
	61(H)	0.003591	0.005083	0.004337	-0.00149

Table S4.	Condensed	Fukui f	functions	calculated	by the	Hirshfeld	charge	population	for the
SA3									

Atom	. <i>f</i> +	f	ſ	Δf
1(C)	0.020678	0.073658	0.047168	-0.05298
2(C)	0.041593	0.070433	0.056013	-0.02884
3(C)	0.067136	0.058663	0.0629	0.008473
4(C)	0.030096	0.119049	0.074573	-0.08895
5(C)	0.039171	0.035886	0.037529	0.003285
6(C)	0.038872	0.04924	0.044056	-0.01037
7(O)	0.012196	0.105435	0.058816	-0.09324
8(C)	0.044482	0.027906	0.036194	0.016576

9(C)	0.040773	0.003513	0.022143	0.03726
10(O)	0.019505	0.0076	0.013553	0.011905
11(C)	0.020396	0.012779	0.016588	0.007617
12(O)	0.055399	0.046345	0.050872	0.009054
13(C)	0.006999	0.00842	0.00771	-0.00142
14(C)	0.004563	0.006698	0.005631	-0.00213
15(C)	0.003861	0.005832	0.004847	-0.00197
16(C)	0.002229	0.00343	0.00283	-0.0012
17(C)	0.00295	0.003219	0.003085	-0.00027
18(C)	0.00254	0.002058	0.002299	0.000482
19(C)	0.00223	0.001625	0.001928	0.000605
20(C)	0.00173	0.001165	0.001448	0.000565
21(N)	0.001128	0.001206	0.001167	-7.8E-05
22(S)	0.002914	0.002029	0.002471	0.000885
23(O)	0.000514	0.000342	0.000428	0.000172
24(O)	0.005944	0.008193	0.007069	-0.00225
25(C)	-0.00028	-0.00126	-0.00077	0.000982
26(C)	-0.00027	-0.00145	-0.00086	0.001181
27(C)	0.00142	0.000735	0.001078	0.000685
28(C)	0.004295	0.00303	0.003663	0.001265
29(C)	0.002653	0.000974	0.001814	0.001679
30(C)	0.004997	0.003561	0.004279	0.001436
31(C)	0.002819	0.000911	0.001865	0.001908
32(H)	0.058512	0.035631	0.047072	0.022881
33(H)	0.053348	0.038818	0.046083	0.01453
34(H)	0.026436	0.047017	0.036727	-0.02058
35(H)	0.061166	0.02965	0.045408	0.031516
36(H)	0.064889	0.029658	0.047274	0.035231
37(H)	0.047561	0.029485	0.038523	0.018076
38(H)	0.018437	0.010603	0.01452	0.007834
39(H)	0.023495	0.014737	0.019116	0.008758
40(H)	0.018237	0.013582	0.01591	0.004655
41(H)	0.017285	0.016774	0.01703	0.000511
42(H)	0.009683	0.01528	0.012482	-0.0056
43(H)	0.002188	0.004495	0.003342	-0.00231
44(H)	0.007286	0.005209	0.006248	0.002077
45(H)	0.005015	0.006616	0.005816	-0.0016
46(H)	0.007728	0.00768	0.007704	4.8E-05
47(H)	0.003219	0.002704	0.002962	0.000515
48(H)	0.003493	0.003623	0.003558	-0.00013
49(H)	0.004298	0.003895	0.004097	0.000403

50(H)	0.006526	0.003282	0.004904	0.003244
51(H)	0.00265	0.002169	0.00241	0.000481
52(H)	0.00643	0.001766	0.004098	0.004664
53(H)	0.005308	0.001441	0.003375	0.003867
54(H)	0.003323	0.002125	0.002724	0.001198
55(H)	0.003324	0.001316	0.00232	0.002008
56(H)	0.002963	0.001056	0.00201	0.001907
57(H)	0.002279	0.001147	0.001713	0.001132
58(H)	0.004349	-0.00151	0.001422	0.005855
59(H)	0.010821	0.002907	0.006864	0.007914
60(H)	0.008929	0.000993	0.004961	0.007936
61(H)	0.009477	0.002948	0.006213	0.006529
62(H)	0.004924	0.002699	0.003812	0.002225
63(H)	0.003601	-0.00052	0.001539	0.004124
64(H)	0.002922	0.001357	0.00214	0.001565

Table S5. Condensed Fukui functions calculated by the Hirshfeld charge population for the SA4

Atom	$f^{\scriptscriptstyle +}$	f	f•	Δf
1(C)	0.020551	0.073426	0.046989	-0.05288
2(C)	0.04136	0.069336	0.055348	-0.02798
3(C)	0.065436	0.058865	0.062151	0.006571
4(C)	0.028802	0.11841	0.073606	-0.08961
5(C)	0.038058	0.035545	0.036802	0.002513
6(C)	0.038433	0.050227	0.04433	-0.01179
7(O)	0.012007	0.105606	0.058807	-0.0936
8(C)	0.041414	0.027941	0.034678	0.013473
9(C)	0.039228	0.003556	0.021392	0.035672
10(O)	0.01916	0.007598	0.013379	0.011562
11(C)	0.017818	0.012799	0.015309	0.005019
12(O)	0.05343	0.046415	0.049923	0.007015
13(C)	0.008312	0.008172	0.008242	0.00014
14(C)	0.00471	0.006274	0.005492	-0.00156
15(C)	0.005742	0.005517	0.00563	0.000225
16(C)	0.002497	0.003049	0.002773	-0.00055
17(C)	0.003954	0.002912	0.003433	0.001042
18(C)	0.003269	0.001747	0.002508	0.001522
19(C)	0.003156	0.001573	0.002365	0.001583
20(C)	0.003321	0.001093	0.002207	0.002228
21(N)	-0.00014	0.000268	6.6E-05	-0.0004

22(S)	0.005796	0.003521	0.004659	0.002275
23(O)	0.004429	0.005886	0.005158	-0.00146
24(O)	0.007354	0.010233	0.008794	-0.00288
25(C)	-0.00109	-0.00153	-0.00131	0.000438
26(C)	0.000871	-8.1E-05	0.000395	0.000952
27(C)	-0.00017	-0.00047	-0.00032	0.000292
28(C)	0.001948	0.001239	0.001594	0.000709
29(C)	0.002836	0.001887	0.002362	0.000949
30(C)	0.002407	0.002221	0.002314	0.000186
31(C)	0.003257	0.001085	0.002171	0.002172
32(H)	0.054412	0.03535	0.044881	0.019062
33(H)	0.051839	0.038733	0.045286	0.013106
34(H)	0.027991	0.046894	0.037443	-0.0189
35(H)	0.058331	0.029578	0.043955	0.028753
36(H)	0.058648	0.029551	0.0441	0.029097
37(H)	0.04449	0.029677	0.037084	0.014813
38(H)	0.01577	0.010624	0.013197	0.005146
39(H)	0.01942	0.014734	0.017077	0.004686
40(H)	0.015015	0.013577	0.014296	0.001438
41(H)	0.02242	0.016661	0.019541	0.005759
42(H)	0.012163	0.015117	0.01364	-0.00295
43(H)	0.002504	0.004025	0.003265	-0.00152
44(H)	0.008297	0.005198	0.006748	0.003099
45(H)	0.006243	0.006296	0.00627	-5.3E-05
46(H)	0.016072	0.007704	0.011888	0.008368
47(H)	0.003796	0.002288	0.003042	0.001508
48(H)	0.005	0.00357	0.004285	0.00143
49(H)	0.012342	0.003927	0.008135	0.008415
50(H)	0.005193	0.003011	0.004102	0.002182
51(H)	0.004947	0.002106	0.003527	0.002841
52(H)	0.009202	0.00144	0.005321	0.007762
53(H)	0.005031	0.001709	0.00337	0.003322
54(H)	0.009766	0.002393	0.00608	0.007373
55(H)	0.003196	0.001437	0.002317	0.001759
56(H)	0.012287	0.000742	0.006515	0.011545
57(H)	0.002805	0.000787	0.001796	0.002018
58(H)	0.001872	0.000436	0.001154	0.001436
59(H)	0.001385	-0.00013	0.000627	0.001517
60(H)	0.006126	0.001471	0.003799	0.004655
61(H)	0.00338	0.002029	0.002705	0.001351
62(H)	0.008392	0.002808	0.0056	0.005584

63(H)	0.004324	0.001295	0.00281	0.003029
64(H)	0.002751	0.000527	0.001639	0.002224

Table S6. Condensed Fukui functions calculated by the Hirshfeld charge population for the SA5

Atom	f^+	f	f•	Δf
1(C)	0.020645	0.071933	0.046289	-0.05129
2(C)	0.039376	0.069735	0.054556	-0.03036
3(C)	0.063732	0.056936	0.060334	0.006796
4(C)	0.026908	0.116756	0.071832	-0.08985
5(C)	0.036365	0.035376	0.035871	0.000989
6(C)	0.037567	0.047606	0.042587	-0.01004
7(O)	0.010793	0.103083	0.056938	-0.09229
8(C)	0.030484	0.027291	0.028888	0.003193
9(C)	0.038993	0.003267	0.02113	0.035726
10(O)	0.019217	0.007267	0.013242	0.01195
11(C)	0.016656	0.012478	0.014567	0.004178
12(O)	0.050802	0.04444	0.047621	0.006362
13(C)	0.006837	0.008414	0.007626	-0.00158
14(C)	0.003935	0.006812	0.005374	-0.00288
15(C)	0.003553	0.00602	0.004787	-0.00247
16(C)	0.002342	0.003786	0.003064	-0.00144
17(C)	0.002973	0.003742	0.003358	-0.00077
18(C)	0.004593	0.002625	0.003609	0.001968
19(C)	0.006343	0.002349	0.004346	0.003994
20(C)	0.008278	0.002124	0.005201	0.006154
21(N)	0.000287	-0.00138	-0.00055	0.001666
22(S)	0.004945	0.004784	0.004864	0.000161
23(O)	0.006512	0.01471	0.010611	-0.0082
24(O)	0.008521	0.008931	0.008726	-0.00041
25(C)	-0.00042	-0.00077	-0.0006	0.000348
26(C)	0.002705	0.001642	0.002174	0.001063
27(C)	-0.00025	-0.00181	-0.00103	0.001558
28(C)	0.003306	-0.00068	0.001313	0.003986
29(C)	0.003349	0.002602	0.002976	0.000747
30(C)	0.004569	0.001829	0.003199	0.00274
31(C)	0.001242	-0.00068	0.000282	0.00192
32(C)	0.009458	0.001402	0.00543	0.008056
33(H)	0.043264	0.035064	0.039164	0.0082
34(H)	0.043628	0.037944	0.040786	0.005684

35(H)	0.021772	0.046063	0.033918	-0.02429
36(H)	0.04083	0.029049	0.03494	0.011781
37(H)	0.031723	0.028909	0.030316	0.002814
38(H)	0.044125	0.028945	0.036535	0.01518
39(H)	0.01334	0.013206	0.013273	0.000134
40(H)	0.018467	0.01442	0.016444	0.004047
41(H)	0.014845	0.010376	0.012611	0.004469
42(H)	0.015127	0.016415	0.015771	-0.00129
43(H)	0.010174	0.015132	0.012653	-0.00496
44(H)	0.005744	0.005211	0.005478	0.000533
45(H)	0.001963	0.004603	0.003283	-0.00264
46(H)	0.004442	0.006702	0.005572	-0.00226
47(H)	0.006784	0.007647	0.007216	-0.00086
48(H)	0.005792	0.003733	0.004763	0.002059
49(H)	0.002351	0.003045	0.002698	-0.00069
50(H)	0.006652	0.004042	0.005347	0.00261
51(H)	0.00613	0.003605	0.004868	0.002525
52(H)	0.004121	0.001968	0.003045	0.002153
53(H)	0.017944	0.002359	0.010152	0.015585
54(H)	0.014814	0.002414	0.008614	0.0124
55(H)	0.019725	0.002549	0.011137	0.017176
56(H)	0.015251	0.004694	0.009973	0.010557
57(H)	0.02181	0.001604	0.011707	0.020206
58(H)	0.028263	0.000667	0.014465	0.027596
59(H)	0.003524	0.001995	0.00276	0.001529
60(H)	0.004831	-0.00053	0.002153	0.005357
61(H)	0.004899	0.00184	0.00337	0.003059
62(H)	0.004464	0.002053	0.003259	0.002411
63(H)	-0.00029	-0.00361	-0.00195	0.003312
64(H)	0.001799	-0.00093	0.000434	0.002731
65(H)	0.007774	0.000719	0.004247	0.007055
66(H)	0.01896	0.002492	0.010726	0.016468
67(H)	0.01445	0.002821	0.008636	0.011629

Ligand	Receptor	Interaction	Distance
	_		(Å)
SA1	ASP158	H-Bond	2.35
	TRP177*	π - π Stacked	5.42
SA2	CYS25*	H-Bond	3.54
	ALA136	Hydrophobic	4.99
	ASP158	π -Anion	4.38
	TRP177*	π - π Stacked	5.55
	TRP177*	Amide- π	4.58
		Stacked	
SA3	ARG8	Hydrophobic	4.90
	VAL13	H-Bond	3.68
	ALA15	Hydrophobic	5.08
SA4	MET142	π -Sulfur	5.05
	TRP177*	π - π Stacked	3.89
	TRP177*	π-Sigma	3.70
	GLN180	H-Bond	3.58
SA5	CYS56	Hydrophobic	4.05
	LYS58	H-Bond	2.40
	CYS63	H-Bond	2.24
	SER64	H-Bond	3.60
	TRP74	Hydrophobic	4.88
	CYS95	Hydrophobic	4.46
	CYS95	Hydrophobic	5.08
A0	ASP18	H-Bond	2.62
	GLY20	H-Bond	2.60
	MET142	π -Sulfur	5.38
	TRP177*	π - π Stacked	4.27
BZN	CYS25*	Hydrophobic	4.99
	TRP177*	π - π Stacked	3.82

Table S7: Types of interactions and distances (Å) between the ligands and the amino acid residues of cruzain.

CONCLUSION

The SA1-SA5 molecules studied in this work were geometrically optimized by performing DFT using B3LYP/6-311+G (d, p) combinations. The IR and NMR spectroscopy data obtained from the calculations were compared with the experimental data in Reddy's article. The comparison was used by linear regression, checking the theoretical-experimental R2 values. The correlation data showed a minimum of 0.9961 and a maximum of 0.9991, indicating excellent structural correlations of the calculated geometries. The study of local and global reactivity of the derivatives was also performed. The data indicated that the SA1 molecule tended to be the most reactive, while the SA2 molecule tended to be more stable. From the analysis of the boundary orbitals, it was observed that the HOMO orbital of the derivatives was concentrated in the A ring region. While the LUMO orbital, the SA1 molecule, was concentrated on ring A, and the substitution of ring B by an aromatic group influenced the LUMO orbital to spread out on ring B. In the local reactivity analysis, described by the isosurface of the electronic function of Fukui, the region responsible for the nucleophilic and electrophilic attack of the molecule was in ring A, highlighting the ordinary atoms among the derivatives: C3, C5, C8, C9, O10, C11, O12, C18, C19, C20, favoring nucleophilic attack of the molecules, and the atoms: C1, C2, C4, C6, O7, C13, C14, C15, C16, C17, favoring electrophilic attack of the molecules. The MESP indicated that the highest electronic concentration, highlighted by red color, was in the ring A region and the Oxygens of sulfonamide, while the methyl region of the methoxyl group of ring A indicated a lower electronic concentration.

From the molecular docking analysis, the interaction SA1-5 with the enzyme 1F29 observed good interaction energy values, being SA1, SA3, and SA4, with values very close to AA. According to articles, it was verified interaction experimentally. The interaction length values of the derivatives SA1, SA2, and SA4 at the Tpr 177 site were excellent compared to AA. Moreover, at the Asn 175 site, they showed values close to or better than BZN. From the 2D map, the SA1, SA2, and SA4 molecules indicated interactions with the Tpr 177 site, AA, and the BNZ, by pi-stacked, revealing the importance of this region for interactions. These interactions corroborate the global and local reactivity data, where the HOMO orbital and the Fukui function isosurfaces indicated reactivity in this ring.

The molecular dynamics calculations were performed to verify the stability of the molecules in the enzyme cruzaina. The results of interaction energy indicated that the complex 1F29-SA4 had the highest interaction energy -179.217 (kj.mol⁻¹) about the others, followed by

the complex 1F29-SA1. Between 1F29 and SA4, there are three hydrophobic interactions with Trp 177 and His 159 (distance of 3.74 Å, 3.75 Å, and 3.94 Å, respectively); Moreover, two hydrogen bonds uncharged of moderate strength were registered with the amino acids Gln 19 (1.82 Å), His 159 (2.05 Å), and a weak one with Trp 177 (2.50 Å).

From this perspective, this study obtained promising results, indicating an excellent interaction of sulfonamide derivative from anacardic acid (SA4) with cruzain, and is recommended for future in vitro testing studies.

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APPENDIX A – AUTHOR'S CURRICULUM DATA



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Projetos de pesquisa

2018 - Atual	CARACTERIZAÇÃO IN SILICO E AVALIAÇÃO DO POTENCIAL FOTOPROTETOR E ANTIOXIDANTE DE EXTRATO DE CLADÓDIOS E SEMENTES DO FRUTO DA HYLOCEREUS
	 DIRUATUS (FITRIA) Descrição: Descrição: As cactáceas são compostas por um grupo de plantas abundantes nas regiões do semiárido. Apresentam bastante especificidade com relação ao seu habitat e possuem diversas adaptações morfológicas e fisiológicas que permitem a sua sobrevivência em ambientes com déficit em nutrientes e água, além de suportar intensa radiação solar. Muitas espécies de cactáceas produzem frutos comestíveis, como as trepadeiras dos gêneros Hylocereus. No Brasil, existem pequenas áreas para produção de pitaya (cactáceas dos Gêneros Hylocereus e Selenicereus). Atualmente, a região Sudeste do Brasil é a principal produtora do país, mas existem diversos plantios distribuídos por todo o país, sendo alguns desses na região da Chapada do Apodi, nos municípios de Limoeiro do Norte e Quixeré, no estado do Ceará. Muitos princípios ativos sintetizados pelas plantas, exercem diferentes funções no vegetal, como atividade antifúngica, antibactericida, antioxidante e fotoprotetora. Com a crescente preocupação sobre os efeitos detetérios ocasionados pela exposição da pele aos raios ultravioleta, torma-se de grande importância a exploração de testes in vitro capazes de caracterizar as propriedades de um protetor ou testar substâncias com princípios ativos que possam vir a ser utilizados como fotoprotetores. A metodologia a ser empregada, compreende a coleta e obtenção do extrato bruto do material vegetal (cladódios e sementes dos frutos da Hylocereus undatus); análise da capacidade antioxidante pelo método DPPH e capacidade dos extratos como fator de proteção solar - FPS in vitro, caracterização estrutural (comprimentos de ligação), eletrônica (orbitais atômicos) e energética (energia de ligação)) dos componentes bioativos, principalmente, pigmentos e compostos fenólicos (metabólitos secundários), presentes no fruto e na polpa, utilizando a teoria do densidade funcional (DFT). Neste contexto, o presente projeto visa caracterizar e avaliar o potencial fotoprotetor e antioxidante do extrat
Áreas de atuação	
1.	Grande área: Ciências Exatas e da Terra / Área: Química / Subárea: Físico- Química/Especialidade: Química Teórica.
Idiomas	

Inglês

Compreende Razoavelmente, Fala Pouco, Lê Bem, Escreve Pouco.

Fielinos e títulos	Prê	èmic	os e	títul	los
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2019	Diploma de Honra ao mérito pela aprovação em 9º lugar na modalidade Química
	Inorgânica na Olimpíada Cearense do Ensino Superior de Química, Universidade Federal do
	Ceará.
2019	Diploma de Honra ao mérito pela aprovação em 7º lugar na modalidade Físico-Química na
	Olimpíada Cearense do Ensino Superior de Química, Universidade Federal do Ceará.
2019	Diploma de Honra ao mérito na classificação geral da Olimpíada Brasileira do Ensino
	Superior de Química, Programa Nacional de Olimpíadas de Química.
2019	Diploma de Honra ao mérito pela aprovação em 21º lugar na modalidade Química
	Inorgânica na Olimpíada Brasileira do Ensino Superior de Química, Programa Nacional de
	Olimpíadas de Química.
2012	1º Lugar Olimpiada Interna de Química, Colégio Santa Isabel.

Produções

Produção bibliográfica

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Ordenar por

Orden	n Cronológica 🗸
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- 2.
- IX Semana Da Química UFC. 2019. (Congresso). XXIII Semana Universitária da UECE.ESTUDOS INICIAIS DE CARACTERIZAÇÃO ESTRUTURAL DA MOLÉCULA MONO(2-3. ETILHEXIL)FTALATO. 2018. (Encontro).
- III ENCONTRO INTERNACIONAL DE JOVENS INVESTIGADORES (EDIÇÃO BRASIL). Estudo DFT do Alcalóide Dincentrina: 4. GAP, HOMO, LUMO, MESP E MULLIKEN. In: III Encontro Internacional de Jovens Investigadores. 2017. (Encontro).
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APPENDIX B – PAPERS PUBLISHED

Physical Chemistry Chemical Physics





Sulfonamide derived from anacardic acid as potential antisores: a theoretical approach based on Molecular Docking, Molecular Dynamics, and Density Functional Theory calculations

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Characterization of the structural, spectroscopic, nonlinear optical, electronic properties and antioxidant activity of the N-{4'-[(E)-3-(Fluorophenyl)-1-(phenyl)-prop-2-en-1-one]}-acetamide



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ABSTRACT

The molecule N-{4'-[(E)-3-(Fluorophenyl)-1-(phenyl)-prop-2-en-1-one]} chalcone (PAAPFBA) was recently synthesized due to the growing interest in the chemistry of the chalcone. The quantum chemical calculations were carried out to make a complete theoretical characterization (structural, spectroscopy, nonlinear optical, and electronic properties) employing three Density Functional Theory (DFT) methods like B3LYP, mPW1PW91, and M06–2X at 6-311++G(d,p) basis set. After all these characterizations, the antioxidant activity was studied using the reaction with the compound DPPH in methanol solution and the mechanism was investigated theoretically. All the three DFT methods used can describe with great accuracy the PAAPFBA chalcone: the results of infrared spectroscopy and the ¹H and ¹³C isotropic shielding demonstrate to be in excellent agreement with the experimental data. The nonlinear optical (NLO) properties show that the title chalcone can be used with great potential in NLO devices and this result is in good agreement with the Natural Bond Orbital (NBO) analysis, which shows how the electronic density is delocalized within the molecule. Finally, the experimental data of the antioxidant ac-tivity showed a moderate rate of reaction with the DPPH molecule (50.92%) and this fact was proved by the theoretical mechanisms with the Hydrogen Atom Transfer (HAT) mechanism more favorable. © 2020 Elsevier B.V. All rights reserved.

1. Introduction

Chalcones are natural products considered as the most important subgroup of the flavonoid family. They are chemically char-acterized by the presence of an open chain with two phenyl rings bonded by α,β -unsaturated carbonyl group (1,3-diphenyl-2propen-1-ones). For the chalcones, there are two possible

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isomers, the E (trans) and Z (cis), being that E isomer occurs naturally and it is thermodynamically more stable [1]. The greatest interest in this class of compound lies in the fact that chalcones have many hydrogen atoms that can be replaced, thus generating the possibility of synthesis routes for several compounds with different possible applications. The chalcone can be used as antileishmanial, antibacterial, antimicrobial, immunosuppressive, antidepressant, anti-inflammatory, anti-obesity, hypnotic, and anticancer [1-11].

Despite these several applications, the chalcones exhibits antioxidant properties. Some examples about the great applicability of chalcone derivatives as antioxidants are given next. Arif et al. [12] studied the antioxidant properties of the 3-(1H-indol-3-yl)-1-p-

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Research article

Quantum computational investigations and molecular docking studies on amentoflavone



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ARTICLE INFO

ABSTRACT

Keywords: Antichagasic agent Biflavonoid DFT Fukui analysis NLO Chagas disease is a neglected tropical disease caused by the protozoan parasite *Trypanosoma cruzi*, with approximately 6–7 million people infected worldwide, becoming a public health problem in tropical countries, thus generating an increasing demand for the development of more effective drugs, due to the low efficiency of the existing drugs. Aliming at the development of a new antichagasic pharmacological tool, the density functional theory was used to calculate the reactivity descriptors of amentoflavone, a biflavonoid with proven anti-trypanosomal activity in vitro, as well as to perform a study of interactions with the enzyme cruzain, an enzyme key in the evolutionary process of *T-cruzi*. Structural properties (in solvents with different values of dielectric constant), the infrared spectrum, the frontier orbitals, Fukui analysis, thermodynamic properties were the parameters calculated from DFT method with the monomeric structure of the apigenin used for comparison. Furthermore, molecular docking studies were performed to assess the potential use of this biflavonoid as a pharmacological antichagasic tool. The frontier orbitals (HOMO-LUMO) study to find the band gap of compound has been extended to calculate electron affinity, ionization energy, electronegativity electrophilicity index, chemical potential, global chemical hardness and global chemical softness to study the chemical behaviour of compound. The optimized structure was subjected to molecular Docking to characterize the interaction between amentoflavone and cruzain enzyme, a classic pharmacological target for substances with anti-gas activity, where significant interactions were observed with amino acid residues from each one's catalytic sites enzyme. These results suggest that amentoflavone has the potential to interfere with the enzymatic activity of cruzain, thus being an indicative of being a promising antichagasic agent.

1. Introduction

Chagas disease is a tropical disease caused by the protozoan parasite *Trypanosoma cruzi*, classified as neglected by the World Health Organization. The Chagas disease is transmitted to humans by the triatomine insect, popularly known, in Brazil, as the barber [1]. Currently, there are approximately 6–7 million infected people in the world and it is estimated that 70 million people will be able to contract this disease. This is an endemic disease in Latin America, Africa and Asia, but also found in

non-endemic developed countries such as Canada, Spain, Japan and Australia [2,3]. Currently, benznidazole and nifurtimox are the only drugs used for the pharmacological treatment of Chagas disease, developed almost fifty years ago, have limited effectiveness in the chronic phase of the disease. However, these drugs led to the occurrence of several side effects, such as polyneuritis, bone marrow depression, lymphoma and dermatitis [4].Therefore, it is necessary to look for new bioactive substances, as well as therapeutic strategies that promote

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ARTICLE

Materials and Corrosion

A theoretical and experimental study of phosphate ester inhibitors for AISI 1018 in carbon dioxide-saturated 3.5 wt% NaCl solution

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1 | INTRODUCTION

Corrosion caused by CO₂ in the aqueous phase is a common problem in carbon steel pipelines used in oil and gas transportation. The formation of corrosion products is usually an essential process in the CO₂ corrosion mechanism, and their presence can significantly change the corrosion rate.^[1,2] For the cathodic process, some papers have proposed two mechanisms: the buffering effect,^[5–7] which relates the impact of the pH on the dissociation of carbonic acid and hydrogen evolution, from a combination of H+, H₂CO₃⁻, HCO₃⁻, and H₂O.^[3,4,8–10] However, steel dissolution accounts for the anodic process.

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Abstract

Phosphate ester was investigated as a corrosion inhibitor for AISI 1018 carbon steel in carbon dioxide-saturated chloride solutions at different temperatures and pressures. The corrosion tests were realized by electrochemical techniques, weight loss measurements, bubble tests, and a high-pressure/high-temperature autoclave system. The corrosion tests demonstrated that the investigated molecule is an excellent corrosion inhibitor. The inhibiting effect is even bigger at high pressure and temperature than at atmospheric pressure and room temperature. The thermodynamic parameters were calculated and determined to obey the Langmuir isotherm. Polarization studies revealed that the evaluated inhibitor is a mixed type.

KEYWORDS

carbon dioxide, corrosion inhibitors, phosphate ester, temperature, pressure

In 1996, Nesic et al.^[11] proposed different anodic mechanisms for steel dissolution in CO₂ solutions at a pH range from 2.5 to 6. The author proposed six reactions at pH < 4, 4 < pH < 5, and pH > 5 (Equations (1)–(6)). Then, for carbon steel, CO₂ corrosion rates are strongly influenced by many factors, such as flow velocity, temperature, pH, gas–liquid rates, oil–water ratio, CO₂ partial pressure, and chemical composition of the produced water^[12–14]:

 $Fe + CO_2 \leftrightarrow FeCO_{2ads},$ (1)

 $FeCO_{2ads} + H_2O \leftrightarrow FeHCO_{3ads} + H^+ + e^-$, (2)

$$FeHCO_{3ads} \leftrightarrow FeHCO_{3ads}^+ + e^-,$$
 (3)

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Full Length Article

Effect of additives on the oxidative stability and corrosivity of biodiesel samples derived from babassu oil and residual frying oil: An experimental and theoretical assessment

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ARTICLEINFO	ABSTRACT
A R T I C L E I N F O Keywords: FUKUI index DFT PDA IONOL Hydrogenated cardanol	The objective of this work is to evaluate the effect of the addition of N,N'-di-sec-butyl-p-phenylenediamine (PDA), IONOL, and hydrogenated cardanol (HC) (500 mg/kg, each) on the oxidative stability and corrosivity of biodiesel obtained from babassu oil (BB) and from residual frying oil (BRFO). Oxidative stability was assessed by induction period (IP) using the Rancimant method (EN 14112), while the corrosivity was assessed by the mass losses of copper coupons immersed in the biodiesel samples (ASTM TM0169/G31-12a (2010)). The most severe corrosion was observed for the fresh biodiesel samples without any additives (4.85 mp) for BB, and 5.00 mp for BRFO). Using PDA, IONOL, and HC as additives inhibited the copper corrosion in both biodiesel samples (between 0.61 and 3.09 mpy for BB, and between 2.19 and 4.69 mpy for BRFO). The use of IONOL and PDA as additives, besides showing a decrease in corrosion rates, also improved the oxidative stability (IP values) for both biodiesel samples (by 66 and > 100 h, for BB; and by 3.31 and 7.23 h, for BRFO, respectively), demonstrating that these additives have bi-functionality in these biodiesel samples. Conversely, the use of HC increased the oxidative stability for BB (by 10.82 h) but also presented a pro-oxidant effect on biodiesel obtained from residual frying oil, decreasing its IP value by cc. 18%. Finally, theoretical studies were carried out based on the formalism of the functional density theory, which confirmed that PDA has indeed the highest anti-corrosion potential among the studied additives.

1. Introduction

The gradual depletion of fossil fuel reserves, the increase of oil prices, and environmental concerns have accelerated the need to find fuels that meet technical and sustainable requirements given the consequences of the greenhouse effect on human health. In this perspective, based on the principles of green chemistry for the use of renewable energies, biodiesel has stood out as an alternative to petrodiesel. This fuel is biodegradable and may be produced from different fatty raw materials [1,2].

Considered environmentally friendly because it is sulfur-free, nontoxic, and derived from renewable sources, biodiesel is however susceptible to oxidation, and this represents one of the biggest challenges in its production and commercialization [3]. In the production of biodiesel, triacylglycerols are converted into esters by transesterification to obtain a fuel that has properties similar to petrodiesel [4]. Among the main advantages, it possesses higher flash point than petrodiesel, which facilitates its transport [5], is biodegradable, and generates fewer emissions [6].

However, due to its chemical structure and the presence of double

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RESEARCH ARTICLE

Synthesis of a new quinine dimer biocatalysed by the coconut water

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ABSTRACT

The obtaining of bis-quinine, a novel alkaloid dimer, has been successfully achieved starting from quinine and the raw coconut juice (Cocos nucifera) as biocatalyst dimerization-like reaction, in mild conditions, with a mass yield of 64.7% in 72 h. The structural elucidation was made based on the spectral data, mainly by a high-field NMR and a mass spectrometry. In a second step, theoretical calculations were performed, an optimised energy structure of the new compound was obtained, the energy gap of the boundary orbitals (HOMO and LUMO) as well as the chemical reactivity descriptors were estimated.

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Quinine; biotransformations; crude enzyme; coconut water

GRAPHICAL ABSTRACT

1. Introduction

In the recent decades, the current model of economic, scientific and technological development, combined with unrestrained consumerism, has generated a significant increase in the consumption of goods and raw materials, as well as an unbridled growth in industrial production and the usage of synthetic chemicals (Chi et al. 2019). This actions have generated an unseen picture of environmental degradation leading to an environmental crisis. Therefore, It is necessary to develop processes and actions that would minimise the harmful entropic effects in the natural and human environments (Faber et al. 2019; Schwarz 2017).

With the purpose to maintain and improve the quality of life around the planet and considering the need for continuous sustainable economic, social and environmental developments, a new chemical conduct would become imperative for the improvement of the techniques and methodologies with the rising generation of toxic residues and effluents. This particular trend, known as Green Chemistry, can be defined as "the creation, development and application of

chemicals, as well as the processes to reduce or eliminate the use in the generation of substances that are harmful to human health and the environment" (Iravani 2011: Lazar 2008: Lewandowski 2014), Hence, this previously mentioned way, provides enzymes that will increasingly replace many conventional catalysts, since they are a sustainable path, because they are ecologically more viable. The usage of enzymes (isolated from vegetables or microorganisms) as catalysts to promote specific changes in a given substrate, is known as biocatalysis, which is considered an interdisciplinary area by correlating studies in organic chemistry and biology, therefore, contributing to the development of new synthetic strategies with the use of easily accessible raw materials (Sheldon and Woodley 2018).

Previous studies have reported the presence of enzymes in all parts of fruits that have been used as biocatalysts in several organic reactions (Chittamuru et al. 2016). Research continues to find sources of enzymes in the Brazilian plants for a later use in biocatalysis, such as the juice of Cocos nucifera L. Among

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ORIGINAL PAPER



A potential bio-antioxidant for mineral oil from cashew nutshell liquid: an experimental and theoretical approach

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Abstract

The objective of the present work was to evaluate the antioxidant potential of a mixture of saturated, monoene, diene, and triene cardanols derived from the cashew nutshell liquid in naphthenic mineral oil. A mineral naphthenic oil sample was doped with the cardanols mixture at concentrations of 500, 2000, and 5000 mg/kg and evaluated using differential scanning calorimetry (DSC) and the accelerated oxidative method (PetroOXY), following ASTM standards (E2041-18, E1970-16, E537-12, and E698-18). The addition of cardanols increased the oxidative stability of the mineral oil by a factor of 4 to 5. To evaluate the antioxidant potential of each particular cardanol present in the mixture, structural analysis and specific antioxidant mechanisms were investigated by density functional theory (DFT). Each molecular structure was optimized with the hybrid functional B3LYP with a basis set 6-31G (d, p), and the antiradical mechanisms (HAT, SPLET, and SET-PT) were evaluated. The HAT was the best observed mechanism, standing out for the cardanol monoene that showed presented better antiradical activity. Concerning the global reactivity study, it was concluded that the increase of the unsaturations in the side chain of the molecules contributes significantly to their increased general reactivity. When evaluating the Fukui index, it was confirmed that, for the cardanol monoene, the reactivity prevails in the aromatic ring with an emphasis on oxygen

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Antioxidant and anticholinesterase activities of amentoflavone isolated from *Ouratea fieldingiana* (Gardner) Engl. through *in vitro* and chemical-quantum studies

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ABSTRACT

Ouratea fieldingiana, popularly known as batiputá, is a tree species easily found in the coastal part of northeastern Brazil. Its leaves are rich in biflavonoids, its major compound being amentoflavone. Biflavonoids are well studied due to their high antioxidant capacity. Alzheimer's disease (AD) is a disease characterized by the progressive loss of neurons. Currently, the pharmacological treatment of AD has four drugs: donepezil, galantamine, rivastigmine and memantine. Where these drugs, with the exception of memantine, are inhibitors of acetylcholinesterase, thus inhibiting the enzyme that destroys acetylcholine, thus increasing the availability of this neurotransmitter. This article aims to determine *in vitro* and *in silico* the antioxidant and anticholinesterase action of amentoflavone isolated from the leaves of Ouratea fieldingiana. The antioxidant capacity of amentoflavone was evaluated using the DPPH⁺ free radical scavenging method, with an IC₅₀ of 5.73 ± 0.08 µg/mL. The antiradical properties of the molecule were also studied *in silico* through several HAT, SET-PT and SPLET mechanisms (HAT) the best trend was obtained as an anti-radical mechanism. Amentoflavone has the ability to inhibit acetylcholinesterase when tested *in vitro*, having an IC₅₀ of 8.68 ± 0.73 µg/mL, corroborating its projection of the *in silico* test, presenting four strong covalent hydrogen bonds for having a bond length up to 2.5 Å. Thus, amentoflavone is an important target for further testing against Alzheimer's disease.

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KEYWORDS

Amentoflavone; antioxidant; density functional theory; enzymes; natural products; quantum chemical calculations



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